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Chan, Christina

Sent: To:

Tuesday, February 07, 2006 7:28 PM Basi, Nirmal; STIC-Biotech/ChemLib RE: Rush search for App. #: 10/083,168

TSubject:

Please rush Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message----

From:

Basi, Nirmal

Sent: To:

Tuesday, February 07, 2006 7:27 PM

Chan, Christina

Subject:

Rush search for App. #: 10/083,168

Thurman I am seeking approval for a RUSH sequence search for an amended case, as

indicated below. If approved, could you

please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi

Art Unit 1646

Office: Remsen Building, Room 4D68 Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/083,168. Result format: Paper.

Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-**COUPLED RECEPTORS**

Inventors:Liaw et al

Priority Date: 4/14/97 Please search:

i) SEQ ID NOs:16, 84 and 85

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed: 7-13-06
Searcher Prep Time:
Online Time:

Type	of Search
NA#	_ AA#:
	ligomer:
Encode/Tran	
Structure #:_	Text:
Inventor:	Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify)

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Search issued, commercial and interference databases.

Thanks, Nirmal S. Basi

Searcher:
Searcher
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Туре	of Search
NA#	_ AA#:
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Structure #:	Text:
Inventor:	Litigation:

Vendors and cost where applicable
STN:
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www/Internet:
Other (Specify):
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us-10-083-168-16.rag.

GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

; Search time 214.5 Seconds (without alignments) 632.951 Million cell updates/sec February 9, 2006, 00:47:19 Run on:

US-10-083-168-16 1614 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
1: geneseqp2004s:*
: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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No.	Score	Match	Match Length	BB	qi	Description
7	1614	100.0	309	e	AAY79576	Human
8	1614	100.0	309	Ŋ	ABG95159	Abg95159 Human GPC
m	1614	100.0	309	9	ABP82002	Abp82002 Human G p
4	1614	100.0	309	7	ADB67656	Human
Ŋ	1614	100.0	309	60	AD029394	Ado29394 Human GPC
•	1614	100.0	309	œ	ADO78094	Ado78094 Human GPR
7	1614	100.0	309	σ	ADV73203	Human
00	1614	100.0	309	σ	AEB15039	
6	1609	99.7	309	Ŋ	ABG95172	Abg95172 Human GPC
10	1608	99.6	309	٣	AAY69989	_
11	1608	99.6	547	7	ADF70461	
12	1606	99.5	309	7	ADF50511	Adf50511 Human GPC
13	1602	99.3	309	٣	AAY58645	Aay58645 Human G-p
14	1602	99.3	309	9	ADA84069	Human
15	1602	99.3	394	80	AD078095	Ado78095 Human GPR
16	1602	99.3	394	80	ADR10454	Adr10454 Human pro
17	1382	85.6	286	00	ADP29765	Adp29765 Human sec
18	1124	69.6	307	80	AD029395	Mouse (
19	402	24.9		7	AAW62597	Human
20	402	24.9	370	'n	ABP61511	Abp61511 Human NF-
21	402	24.9		9	ABG73513	
22	402	24.9	370	9	ABP81870	Abp81870 Human G p
23	402	24.9	370	7	ADH69286	Human
24	402	24.9	370	80	ADF91778	Adf91778 Human P2Y

Ado29049 Human nov	Adq88244 Human 241	Human	Ads84260 Human G p	_	Adf70491 Orphan re	Adh69285 Human pur	Human	Mouse	Abp61510 Human NF-	Human	Ado29415 Mouse GPC	Adw44804 Human RUP	Human	Aeb20962 Human RUP	Human	Human 1	Human R	Adw44805 Human RUP	Adw44814 Human RUP	Aau77993 Human inf
AD029049	ADQ88244	ADQ81575	ADS84260	ADV35123	ADF70491	ADH69285	ADF91777	AD029050	ABP61510	ADS84259	AD029415	ADW44804	ADW44778	AEB20962	ADW44807	ADW44802	ADW44810	ADW44805	ADW44814	AAU77993
370 8	370 8	_	370 8	•	608 7	370 7	370 8	370 8	370 5	368 8	327 8	363 9	_	-	-	363 9	-	363 9		363 5
24.9	24.9	24.9	24.9	24.9	24.9	401 24.8	24.8	24.6	24.3	390 24.2	23.9	23.6	23.6	23.6	23.5		23.4	23.4	23.4	23.3
25	26	27	28	50	í e	31	35	33	3.6	35	36	37	8	3 6	0 4	41	4 2	, 4 , 6	4 4	45

ALIGNMENTS

GPR35; G protein coupled receptor; human; NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10; diagnosis; therapy. Human G protein coupled receptor GPR35. AAY79576 standard; protein; 309 AA. (first entry) 15-AUG-2000 AAY79576;

/note= "encoded by AGT" note= "encoded by GCG" Location/Qualifiers Key Misc-difference 174 Misc-difference 294 Homo sapiens.

99WO-US024890. 98US-0105052P. 99US-0134175P. WO200023603-A2 21-OCT-1998; 13-MAY-1999; 21-OCT-1999; 27-APR-2000.

Otani K; Zhon Y, Sreenan S, ž Oda S, Horikawa Y, Oo Bell GI, Cox NJ; Polonsky KS, Hanis CL, Be

(ARCH-) ARCH DEV CORP. (TEXA) UNIV OF TEXAS SYSTEM.

WPI; 2000-339702/29. N-PSDB; AAA27485, AAY79574, AAY79576.

Method for screening for type 2 diabetes mellitus comprises detecting a polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.

Claim 75; Page 237-238; 257pp; English.

The present sequence is that of the human gene encoding G protein coupled

us-10-083-168-16.rag

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receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The sequence of GPR35 is similar to that of a putative purinoceptor PYY9 (a14.14 identity) suggesting that ATP or other nucleotide is its ligand. GPR35 mRNA was detected in all adult and foetal tissues examined with relatively higher levels in adult lung, small intestine, colon and roumach. In these tissues, there are Z major transcripts of 2.4 and 4.4 kb, whereas in skeletal muscle there is a single transcript of 9.4 kb. The GR835 gene is located in a 49,136 bp region (see AAA27475) within the NIDDM1 region of human chromosome 2. This region also includes the CAPN10 gene, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CAPN10 gene are responsible for greened to type 2 diabetes calpain-like cysteine protease, designated propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a propensity for type 2 diabetes mellitus are based on detection of a mudulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport
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Sequence 309 AA;

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61 NLAVADLCTLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                        61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                            PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
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                                                                                       1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVPCCRMQQWTETRIYMT
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                                                                  1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                     Gaps
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 Length 309;
                                   0; Indels
100.0%; Score 1614; DB 3; 100.0%; Pred. No. 3.1e-167;
                                   0, Mismatches
                                  Matches 309; Conservative
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                 Best Local Similarity
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ABG95159 standard; protein; 309 AA. (first entry) Human GPCR GPR35 04-DEC-2002 ABG95159 RESULT

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor.

Homo sapiens

WO200268600-A2

06-SEP-2002

26-FEB-2002; 2002WO-US005625.

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181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARNWANLLVFVVCFLPLHVGLTVR 240
                                                                                                                                                                                                                                                                                                                                                                                           New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reflux disease, depression, migraîne, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, ansesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present sequence represents an endogenous human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polymucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQG1YLTNRYMS1SLVTAIAVDRYVAVRH
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                                                                                                                                                                              Leonard JN;
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                                                                                                                                                                              Maciejewski-Lenior D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0, Indels
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100.0%; Pred. No. 3.1e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Page 128-130; 201pp; English.
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                             26-FEB-2001; 2001US-0271913P.
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Ortuno D;
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino condition of a particular G acide. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (1) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related diseases, growth-related diseases, call creating immune-related diseases, jemunological-related cell proliferative ciseases, or autoimmune diseases, jemunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, canxiety, depression, schizophrenia, dementia, mental retardation, memory considering yorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ45531 to ABZ42869 encode condition of the present invention
Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown JP;
                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burmer GC, Roush CL,
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N-PSDB; ABZ42852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases.
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                                                                                                                                                                                                                                                            WO200261087-A2
                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                             08-AUG-2002
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Query Match
Best Local Similarity 100.
Matches 309; Conservative
Sequence 309 AA;
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                                                                                                                        MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                        61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIYMT
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                      Length 309;
                                                            IndelB
                      100.0%; Score 1614; DB 6; 100.0%; Pred. No. 3.1e-167;
                                                            0; Mismatches
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Matches 309; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting pathological conditions in heart failure using marker genes
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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS
                                                                                                241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAFRAKHKS
                                    YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
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100.0%; Pred. No. 3.1e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            SEQ ID 25.
                                                                                                                                                                                                                                                                                                                   Cardiant; Gene therapy; heart failure; human;
                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor 35; receptor.
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                                                                                                                                                                                                                                                                                            Human G protein-coupled receptor 35,
                                                                                                                                                                                                                       ADB67656 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002; 2002JP-00054388.
15-APR-2002; 2002JP-00112228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitakaze M, Takashima S,
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                   QDSLCVTLA 309
                                                                                                                                                   QDSLCVTLA 309
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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associated with GPCRs of the invention; methods of screening for
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                                                                                                                                                                                                                                                                                                                                                         Transgenic mouse, neceptor; GPCR; drug screening; diagnosis;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; intestinal disorder; cardiovascular disorder;

colon disorder; blood disorder; immune disorder; bone disorder;

colon disorder; blood disorder; immune disorder; cancer;

concer; metabolic disorder; mutritive disorder; cancer;

concer; metabolic disorder; prostate disorder; cancer;

concer; iterus disorder; prostate disorder; cancer;

concer; scomach disorder; prostate disorder; spleen disorder;

concer; thyroid disorder; antiparkinsonian; antimanic;

cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic;

contral nervous system; respiratory; antidiarrhoeic; antidiabetic;

contral nervous system; respiratory; antidiarrhoeic;

dermatological; antiulcer; antithyroid; antiallergic; antidiabetic;

dermatological; antiulcer; antithyroid; antiallergic; anorectic;

munnosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
                      180
                                                                            240
                                                                                                      LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                                                                                                                      LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKEFQEASALAVAPRAKAHKS 300
                                                              YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMYMANLLVFVVCFLPLHVGLTVR
               PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GA, Bergmann JE, Gragerov A, Hohmann J,
Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                      ADO29394 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                    Human GPCR GPR35, SEQ ID NO:496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2002; 2002US-0409303P.
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                                                                                                                                                                                                                                                                                                        29-JUL-2004 (first entry)
                                                                                                                                                           309
                                                                                                                                                                                     ODSLCVTLA 309
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The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases

Claim 151; SEQ ID NO 496; 542pp; English.

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Sasociated with Garkes of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a compounds useful in the treatment of the invention; a defined of the invention in a different GPCR golymucleous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has comprising a which hybridise to GPCR polymucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid; The GPCR polypeptides and vectors comprising a GPCR nucleic acid; The GPCR polypeptides and vectors comprising a GPCR nucleic acid; The GPCR nucleic acids and proteins may be used in the disgnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, distributions of disease or schizophrenia); classification disorders of the adrenal gland; disorders (e.g., Alzheimer's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders; blood disorders (e.g., angina, cardiac arrhythmia or syndrome); cardiovascular disorders; blood disorders (e.g., another disorders or the disorders or the disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid chiesases); and disorders of the kidney, liver, lung, breast, ovary, cobesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases) and disorders of the kidney, liver, lung, breast, ovary, cuterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and chiesase, the kidney, liver, lung, breast, dern part of the present sequence represents a GPCR of the convent of the printed data for this patent did not form part of the convent of the proper of the prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NIAVADLCILCTIPPVIHSIRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVPCCRMQQWTETRIYMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1614; DB 8;
100.0%; Pred. No. 3.1e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 100.
Matches 309; Conservative
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Klein BK;

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New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
           Human colon tumor cell upregulated protein SEQ ID NO
                                                                                                                                                                                                                                                            Bu JJ, Head RD, Hippenmeyer PJ, A, Staten NR;
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 44; 257pp; English.
                                           cancer; neoplasm; cytostatic
                                                                                                                                                                     28-OCT-2003; 2003WO-US034019
                                                                                                                                                                                                   29-OCT-2002; 2002US-0422176P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 309; Conservative
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                                                                                                                                                                                                                                (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                           2005-039958/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                           N-PSDB; ADV73165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 309 AA;
                                                                                                        WO2004110345-A2
                                                                                                                                                                                                                                                                              Mazzarella RA,
                                                                          Homo sapiens
                                                                                                                                       23-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                         The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and monitoring of tumours. The present sequence represents the amino acid sequence of a human GPR35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                              Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKKAHKS
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100.0%; Score 1614; DB 8; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 309; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                  Claim 72; SEQ ID NO 9; 124pp; German
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                                                                                                             22-NOV-2002; 2002DE-01054601
                                                                                                                                          22-NOV-2002; 2002DB-01054601
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                                                                                                                                                                         (GANY-) GANYMED PHARM
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N-PSDB; ADO78086.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 309 AA;
                                               DE10254601-A1
                   sapiens
                                                                               03-JUN-2004
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                                                   The
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                                                                                                                                                                                                                                                                                                                                                                   NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
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                                                                                                                                                                                                                                                                             1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. present sequence represents the amno acid sequence of a protein
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                     100.0%; Score 1614; DB 9;
100.0%; Pred. No. 3.1e-167;
tive 0; Mismatches 0;
                                                                                                 upregulated in human colon cancer cells
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10-MAR-2005 (first entry)

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cardiovascular claims to the use of numan G-protein coupled receptor 35 (GRR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders, in a mammal. Great neurological disorders and urological disorders, in a mammal. Great neurological disorders and urological disorders, in a mammal. Great neurological compound with GPR35 polypeptide, and detecting the binding of the test compound with GPR35 polypeptide, and detecting the binding of the test compound to the polypeptide, and detecting the binding of the test compound to the grass polymelectide in a sample taken from the mammal, and determining the amount of the GPR35 polymelectide in healthy and/or diseased mammals of GPR35 polymelectide in healthy and/or diseased mammals. Comparising a therapeutic agent that binds to the GPR35 polypeptide, (3) use of regulators of a GPR35 for the preparation of the pharmaceutical composition or for the regulation of GPR35 activity or a mammal having the above specified diseases; and (4) a method for the graparation of the pharmaceutical composition, comprising identifying the composition of the regulator ameliorates the symptoms of the above specified diseases; and (4) a method for the symptoms of the above specified diseases; and mammal, and combining the regulator, determining whether the regulator ameliorates the symptoms of the above specified diseases in a mammal, and combining the regulator with an acceptable pharmaceutical camposition of GPR35 and diseases, and gastrointestinal diseases, cancer disorders, inflammatory diseases, neurological disorders and urological disorders, respiratory diseases, neurological disorders and urological disorders in a mammal, e.g. humans (preferably), dogs, cats, cows, horses, rabbits, and monkeys. This
                                                                                           screening; cardiovascular disease; gastrointestinal disease;
liver disease; cancer; neoplasm; metabolic disorder;
hematological disease; respiratory disease; inflammation;
neurological disease; urological disorder; cardiovascular-gen.;
gastrointestinal.gen.; hepatotropic; cytostatic; metabolic; antianemic;
respiratory-gen.; antiinflammatory; neuroprotective; uropathic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to the use of human G-protein coupled receptor 35
                                                                         G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summer H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 2, 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geerts A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-2003; 2003EP-00028614.
                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004; 2004WO-EP013679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER HEALTHCARE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brueggemeier U,
                       GPR35 polypeptide
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                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                          1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                            1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                      Gaps
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Length 309;
                                    Indels
                    3.1e-167;
Match 100.0%; Score 1614; DB 9; Local Similarity 100.0%; Pred. No. 3.1e-167; es 309; Conservative 0; Mismatches 0;
Query Match
                  Best Loca
Matches
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61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, ansesthesia, mycardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostatic cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present sequence represents a mutant human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.
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                                                                          121 PLRARGIRSPROAAAVCAVLWVLVIGSLVARWILGIQEGGFCFRSTRHNFNSWRFPLLGF
                                                                                                                       181 YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCPLPLHVGLTVR
                                                                                                                                              181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARHVWANLLVFVVCFLPLHVGLTVR
                                                      PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human receptor-associated protein; HRAP; Incyte clone 3083742; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiateriosclerotic; hepatotropic; antialerthritic antirhemuatic; antiatesthmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; aethma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.
                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                          YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKÅARNVANLLVPVVCFLPLHVGLTVR 240
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                                                                                                                                                                                                                                                                                  PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                              MIGTYNTCGSSDLTWPPAIKGGFYAYLGVLLVLGLLLNSLALWVFCCRWQQWTETRIYMT
                                                                                                                       1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human receptor-associated protein from Incyte clone 3083742.
                                       Length 309;
                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ./note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Potential phosphorylation site"
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"G-protein_coupled_receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Potential phosphorylation
                                         99.7%; Score 1609; DB 5; 99.7%; Pred. No. 1.1e-166;
                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69989 standard; protein; 309 AA.
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/label= Si
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                                                                                 Matches 308; Conservative
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238
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                                                                 Local Similarity
    Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                         Query Match
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The present sequence is human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUNOI cDNA library. This sequence is expressed in haemacopoietic/immune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiatreriosclerotic, hepatotropic, antianthritic, antiathering, antiathering, antiathering, antiathering, antiathering, antiathering, antiathering anticheumatic, osteopathic, antialergic, antianaemic, antiasthmatic, sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, dutoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRWQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PLRAKGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMAFPLLGF
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                                                                              /note= "Potential phosphorylation site"
              /note= "Potential phosphorylation site"
261
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%; Score 1608; DB 3;
99.7%; Pred. No. 1.4e-166;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 76; 99pp; English.
                                                                                                                                                                                                                                                    99WO-US017777.
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98US-0098703P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yue H, L
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-205710/18.
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                                                                                                                                        WO200008155-A2
Modified-site
                                                       Modified-site
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Corley NC, F
                                                                                                                                                                                                                                                    06-AUG-1999;
                                                                                                                                                                                                                                                                                                           07-AUG-1998;
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                                                                                                                                                                                               17-FEB-2000
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                     Human GPCR GPR35 D113A mutein (SeqID 191).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                       ADF50511 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saeki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2003; 2003WO-JP004840.
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                                                                                                    301 ODSLCVTLA 309
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Obinata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-833737/77.
                                                    301 QDSLCVTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003087366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                        12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishi T,
                                                                                                                                                                                                                                                                         ADF50511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPUV or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCPLPLHVGLTVR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands
                                                                                                                                                                                                                                        ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP; GFPuv; Enhanced GFP; EGFP; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNGTYNTCGSSDLIWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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                                                                                                                                                                                              Orphan receptor ligand-related human protein SeqID84.
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99.64; Score 1608; DB 7;
Best Local Similarity 99.74; Pred. No. 2.8e-166;
Matches 308; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 84; 594pp; Japanese.
                                               ADF70461 standard; protein; 547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2002; 2002JP-00045728.
23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2003; 2003WO-JP001901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LID
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the orphan receptor.
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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RESULT 11

ADF70461

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for obtaining a DNA that encodes
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mutant; mutein; transformation; endocrine cell line;
expression cloning system; bioactive peptide; GPCR ligand; human.
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                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Asp substituted by Ala"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                 GPR35A; human; G-protein coupled receptor; purinergic; 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic; cytosteatic; antidiabetic; anotectic; antiasthmatic; antiparkinsonian; hypotensive; osteopathic; antianginal; cardiant; cerebroprotective; antiuloer; antiallergic; antimigraine; antiemetic; tranquillizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
                               LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS
MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                    NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                             PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                     YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.
                                                                                                                                                                                                                                                                                                                               Human G-protein coupled receptor GPR35A.
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N-PSDB; AAZ35390.
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obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporossis; angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic and neurological disorders including anxiety, schizophrenia, manic depression, dellitium, dementia and severe mental retardation; and dyskinesias such as Huntingdon's or Gilles de la Tourette's syndrome. The polypeptide is also useful for production of vaccines
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Pred. No. 6.3e-166;
0; Mismatches 2;
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22-0CT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
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Best Local Similarity 99.4
Matches 307; Conservative
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N-PSDB; ADA84068.
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                                                                                                                                                                                                          Sequence 309 AA;
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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (BSTB) known to be expressed in the phenotype/cell type of interest with all BSTB expressed in normal tissue in order to identify BSTB that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of phenotype such as hyperosmotic stress or high salt conditions. A method cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful expression for tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a cumour-associated antigen of the invention.
Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                      Claim 29; Page 448-449; 516pp; English.
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Sequence 309 AA;

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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBPQBASALAVAPRAKAHKS 300
                                                                                                                                                                                                        PLRARGLRSPROAAAVCAVLWTVIGSLVARWILGIOEGGFCPRSTRHNFNSMAFPLLGF 180
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                                                                                                                            NLAVADLCILCTLPFVI.HSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                        PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
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                                                                                   MIGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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                                                              1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                               Gaps
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Length 309;
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99.3%; Score 1602; DB 6; 99.4%; Pred. No. 6.3e-166; iive 0; Mismatches 2;
             Best Local Similarity 99.4 Matches 307; Conservative
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tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; proetate cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; GRN35.
              ADO78095 standard; protein; 394 AA
                                                                       (first entry)
                                                                                                  Human GPR35 isoform.
                                                                       26-AUG-2004
                                            ADO78095;
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The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated artigen (TAg) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAg, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAg, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and monitoring of tumours. The present sequence represents the amino acid sequence of a human GPR35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                            Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFORASALAVAPRAKAHKS
126 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYWAKEFORASALAVAPSAKAHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMOOWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDTKYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSWAFPLLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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                                                                                                                                                                                                                                                                                                                              tumor-associated antigens, useful for tre-
compositions for diagnosis and monitoring
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                                                                                                                                                       22-NOV-2002; 2002DE-01054601.
                                                                                                                  22-NOV-2002, 2002DB-01054601,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         WPI; 2004-421820/40.
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                                      DE10254601-A1
    Homo sapiens.
                                                                            03-JUN-2004.
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                          Copyright
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model 3 using protein search, OM protein

9, 2006, 00:55:13 February Run on:

; Search time 26.5 Seconds (without alignments) 1121.924 Million cell updates/sec

US-10-083-168-16 1614 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

вишшатіев

pir1:* pir2:* pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Description			G protein-coupled		G protein-coupled	ATP receptor P2u -		G protein-coupled	bradykinin B2 rece	bradykinin recepto	platelet-activatin	P-2U nucleotide re		G protein-coupled	bradykinin Bl rece	platelet-activatin	G protein-coupled	\sim		G protein-coupled	vat	P2Y6 receptor - hu	angiotensin II rec	chemokine (C-C) re	G protein-coupled	platelet activatin	bradykinin B2 rece		somatostatin recep
	QI	JC5549	I50241	169202	T09508	I55450	A47556	S33733	868679	JQ1488	OORTB2	S13638	A54946	153033	A57641	S60024	A40191	B57641	JC4162	S68207	JC4737	843252	JC4800	JC2543	A43113	B45680	863666	149519	I57955	JN0763
(8	7	~	7	7	~	~	~	~	~				7														~	0	7
•	Match Length	370	308	387	344	328	373	362	365	364	366	342			362		342	362	373	362	373	341	328	363	352	361	341	366	363	364
* Query	Match	24.8	22.8	22.8	22.3	19.8	19.8	_	_	_	_	19.2	19.1	18.9	18.9	18.9	18.8	18.7	18.7	18.7	18.5	18.2	18.0	17.9	17.9	17.7	17.5	17.4	17.3	17.3
,	Score	4	368.5	368.5	360.5	319	319	318	315.5	312.5	312.5	310	308.5	305.5	305.5	305	304	302.5	302.5	301.5	298.5	293	291	289	288.5	285.5	283	281.5	279.5	279.5
Result	No.	ч	8	٣	4	2	ø	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

angiotensin II rec	G protein-coupled	angiotensin II rec	somatostatin recep	macrophage inflamm	thrombin receptor	G protein-coupled	G protein-coupled	HHRF3 protein - hu	somatostatin recep	G protein-coupled	G protein-coupled	chemokine (C-C) re	somatostatin recep	somatostatin recep	somatostatin recep
A49092	JC5653	148261	I57940	149339	151667	T09353	S68208	QQBED3	A46226	JC5067	JC5068	A45177	A41795	C41795	A39297
~	7	7	7	0	~	~	~	н	~	7	~	7	~	N	~
363	361	363	363	355	420	354	365	323	418	355	369	355	391	391	391
•															
	17.1	17.0	17.0	16.9	16.8	16.8	16.7	16.7	16.6	16.5	16.3	16.3	16.3	16.3	16.3
	276.5 17.1				271.5 16.8				268 16.6	266.5 16.5			262.5 16.3		

ALIGNMENTS

heptahelical P2Y5-like receptor - human

Cippedies: How sapiens (man)
Cippedies: How sapiens (man)
Cippedies: How sapiens (man)
Cipates: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
Cipates: 07-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
Cipates: 07-Sep-1997 #sequence_revision 05-Sep-1997
Rights Cipates Res. Commun. 236, 106-112, 1997
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Fitle: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Fitle: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Accession: JC5549; MUD:97366605; PMID:9223435
A;Accession: JC5549; MUD:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 cJAN>
A;Cross-references: UNIPROT: Q99677; UNIPARC: UPI000016A4CA; DDBJ:AF005419; NID:g2240034;
C;Superfamily: ATP receptor P2u

Gaps 42; Length 370; 24.8%; Score 401; DB 2; Length 370 llarity 34.0%; Pred. No. 1.9e-29; Conservative 58; Mismatches 104; Indels Best Local Similarity Matches 105; Conserv Query Match

44 AVYSVVPILGLITNSVSLEVFCFRRKGARSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103 81 25 AYLGYLLVIGLLINSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--ઠે 셤

82 -DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140 104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGV 162 δ

셤

WVLVIGSLVARWILGIQEGGF-----CPR----STRHNFNSMRFPLLGFYL 182 141 ò

163 WILVLSG------GISASLFSTINVNNATTICFEGLSKRVWKTYLSKITIFIEVVGFII 엄

PLAVVVFCSLKVVTALAORPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRL 241 183 ò g 242 AVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAH 298 Š

299 KSQDSLCVT 307 ò g

g

328 IRMESLFKT 336

I50241
G protein-coupled receptor 6H1 - chicken
N,Alternate names: purinoceptor 6H1
C,Species: Gallus gallus (chicken)
C,Species: Ja-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C,Accession: I50241, JC4618

17

Gaps

29;

Indels

Length 387;

141

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infron 17 purinergic receptor P2YS - human
N.Alternate names: G-protein coupled receptor
C,Species: Homo sapiens (man)
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C,Accession: 109508
R,BOhm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A,Description: The human purinergic receptor P2YS is encoded in intron 17 of the retinobla A,Accession: 709508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: P43657; UNIPARC: UPI000005041B; EMBL: AF000546; NID: 92233068; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----N 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 IIWSLRQR---QWDRHAKIKRAITFIMVVAIVPVICPLP---SVVVRIRIFWLLHTSGTQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTALAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 FVFTLPPRIFYF-TTRNWPPGDLLCKISVMLPYTNMYGSILFLTCISVDRFLAIVYPFKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGLRSPRQAAAVCAVLWVLVI-GSLVARMLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 LGLEFIFGLLGNGLALMIFCFFHLKSWKSSRIFLFNLAVADFLLIICLPFVMDYYVRRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 SSHCPYNDSPKYTLYGCMPSMVPVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY
                                                                                                                                                                                                                                     27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPPVL----HSLR
                                                                                                                                                                                                                                                                                                                                                                                     82 DISDIPLCQLSQGIYLINRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALMVFCCRMQQWTETRIYMTNLAVADLC
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Best Local Similarity 29.2%; Pred. No. 1e-25;
Matches 90; Conservative 68; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 NCEVYRSVDLAPFITLSFTYMNSMLDPVVYYFSSPSF 301
                                                                         ch 22.8%; Score 368.5; DB 2; 1 Similarity 34.3%; Pred. No. 2.1e-26; 95; Conservative 48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
       C; Superfamily: G protein-coupled receptor 4
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                                                                             Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-344 < BOH>
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169202
G protein-coupled receptor HM74 - human
C species: Homo sapiens (man)
C species: I species: Homo sapiens (man)
C species: I s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Residues: 1-308 <WEB>
A/Rose-references: UNIPARC: UPI0000055A6B; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID: A/Experimental Bource: T-cells
C/Comment: This receptor plays a role in T-cell activation.
C/Genetics:
A/Gene: p2/S
C/Superfamily: ATP receptor P2u
C/Reywords: G protein-coupled receptor; transmembrane protein
C/Reywords: G protein-coupled receptor; transmembrane #status predicted <TM1>
F/S1-40/Domain: transmembrane #status predicted <TM2>
F/89-109/Domain: transmembrane #status predicted <TM3>
F/33-L53/Domain: transmembrane #status predicted <TM5>
F/177-201/Domain: transmembrane #status predicted <TM5>
F/277-248/Domain: transmembrane #status predicted <TM5>
F/277-248/Domain: transmembrane #status predicted <TM5>
F/269-292/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                   A.Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biochyar, Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: ISO241; MUID:93329058; PMID:8393036
A;Accession: ISO241
A;Accession: ISO241
A;Mulacus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: [1-308 < KAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----PP- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------LIGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SGNCSTEDSFKYTLYGCVFSMVPVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
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Grotein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 833733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnston R;Webb, T.E.; 234, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-362 <MEB>
A;Cross-references: UNIPROT:P34996; UNIPARC:UPI0000405D4; EMBL:X73268; NID:g395084; PI1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 QEGG--FCFRSTRHNF-----NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 RRNKTITCYDTTADBYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYK---DLDN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SPLRRKSIYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 FCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRHN-------FNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPP--TDVGQAE 210
                                                                                                                                                                                                                                                                                                                                                                                             49 MOGWTETRIYMTNIAVADLCLLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSI 104
                                                                                                                                                          105 SLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGEFCFR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                  9 NSTINGTWEGD------ELGYKCRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCR
2 NGTYNTCGSSDLTWPPAIKLGF-----YAYL----GVLLVLGLLLNSLALWVFCCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCLDAICYYY------MAKEFORASALAVAPRAK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 SCLDPVLYFLAGQRLVRPARDAKPPTEPTESPQAR 333
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Matches 96; Conservative
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                                                                                                                    RESULT 5

155450
G protein-coupled P2 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 09-011-2004
C;Accession: 155450
R;Chang, K.; Hanacka, K.; Kumada, M.; Takuwa, Y.
C;Accession: 155450, MulD:96064682; PMID:7592819
A;Accession: 155450
C;Superiaminary: translated from GB/EMBL/DDBJ
A;Accession: 155450
A;Accession: 155450
C;Superiamily: ATP receptor P2u
C;Superiamily: ATP receptor P2u
C;Superiamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFF; GB:L14751; NID:g309457; PIDN
Superfamily: ATP receptor P2u
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession. A.7556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells. A;Reference number: A47556
A;Accession: A4756
A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 KAARWVWANLLVFVVCFLPLHVGLTVRLAVGWN---ACALLETIRRALYITSKLSDANCC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 KAARMAVVVAAVFVISFLPFHITKTAYLAVRSTPGVSCPVLETFAAAYKGTRPFASANSV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 QWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 VTAIAVDRYVAVRHPIRARGIRSPROAA-AVCAVIWVIVIGSIVARWIL---GIQEG-GF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF-----RSTRHNFNSMRPPLLGFYLPLAVVVPCSLKVVTALAQR--PPTDVGQAEATR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NGTY-----NTCGSSD----LIWPPAIKLGFYAYLGVLLVIGLLLNSLALWVFCCRMQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 NGTIQAPGLPPTTCVYREDFKRLLLPPV-----YSVVLVVGLPLNVCVIAQICASRR 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 19.8%; Score 319; DB 2; Length 32
Local Similarity 30.6%; Pred. No. 6.6e-22;
hes 96; Conservative 48; Mismatches 130; Indels
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LDPILFYFTQQKFR 309
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               : | :
294 TSDTIQNS 301
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Best Local Similarity
Matches 101; Conserv
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Best Local Si
Matches 96;
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Reference number: A55559; MUID:95137582; PMID:7835885
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A, Molecule type: mRNA
                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                        Gene: GDB:BDKRB2
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Dradykinin B2 receptor - human
C;Becies: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Bate: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Bate: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Bate: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH0712; A46022; A55559; JQ1488; JG1400
B;Cocken anumber: JH0712; MUID:93038601; PMID:1329734
A;Accession: JH0712; MUID:93038601; PMID:1329734
A;Accession: JH0712
A;Molecule type: DNA
A;Accession: JH0712
A;Aocession: JH0712; MUID:930411; UNIPARC;UPI000002A4FC; GB:S45489; NID:g256536; PIDN: R;Powell: S.J; Slynn, G; Thomas, C.; Hopkins, B; Briggs, I.; Graham, A.
A;Accession: J455-489, 1993
A;Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to chapters and saference number: A46022; MUID:93194199; PMID:7916737
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A;Molecule type: DNA
A;Cross-tracted expons
A;Cross-tracted from NCBI backbone (NCBIN:127280, NCBIP:127284)
A;Note: sequence extracted from NCBI backbone (NCBIN:127280, NCBIP:127284)
B;Ma, J; Wang, D: Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.
Genomics 23, 362-369, 1994
A;Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human brad
G protein-coupled receptor - human
G protein-coupled receptor - human
G protein-coupled receptor - human
C;Specias Homo aspiens (man)
C;Specias Homo aspiens (man)
C;Accession: 868679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expre
A;Reference number: 868679; MUID:96197801; PMID:8617367
A;Reference number: 868679
A;Reference number: Bose FEBS
A;Reference number: Bose FEBS
A;Reference number: Bose FEBS
A;Residues: 1-365 <8TA>
A;Residues: 1-365 <8TA>
A;Residues: 1-365 <8TA>
Crosser-references: UNIPROT:PS1S82; UNIPARC:UPIO00002E776; EMBL:X96597; NID:g1296631; PI
C;Reywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLETIRRALYITSKLSDANCCLDAICYYYMAKEFQE------ASALAVAP 293
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Matches 93; Conserv
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A;Crose-references: GDB:135713; OMIM:113503
A;Amap position: 14q32.1-14q32.2
A;Introns: #status absent
A;Introns: #status absent
C;Superfamily: vertebrate thodopsin
C;Superfamily: vertebrate thodopsin
C;Superfamily: vertebrate absent
F;34-56/Domain: transmembrane #status predicted <TM1>
F;66-92/Domain: transmembrane #status predicted <TM2>
F;104-127/Domain: transmembrane #status predicted <TM3>
F;104-127/Domain: transmembrane #status predicted <TM3>
F;105-221/Domain: transmembrane #status predicted <TM5>
F;241-266/Domain: transmembrane #status predicted <TM7>
F;241-26/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted F;242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted F;316/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted F;316/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
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A;Accession: A55559
A;Molecule type: DNA
A;Residues: 1-364 <MAA>
A;Cross-references: UNIPARC:UDI000002A4FC; GB:L27594
A;Cross-references: UNIPARC:UDI000002A4FC; GB:L27594
B;Chess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Biochem: Biophys. Res. Commun. 184, 260-268, 1992
A;Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor an annual strate of the strate of th
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A;Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID
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C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283; A55079; S47529
R;McBachern, A.E.; Shelton, E.R.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppi
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
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Best Local Similarity 27.6
Matches 89; Conservative
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58;
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31; Conservative
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Matches 81
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A;Residues: 1-366 <MCE>
A;Cross-references: UNIPROT:P25023; UNIPARC:UPI00001708A1; GB:M59967
B;Cross-references: UNIPROT:P25023; UNIPARC:UPI00001708A1; GB:M59967
B;Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
A;Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence A;Reference number: A55079
A;Accession: A55079
A;Status: Preliminary; not compared with conceptual translation
A;Residues: L.75, 'A',77-366 <PRES>
A;Residues: L-75, 'A',77-366 <PRES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA

A, Residues: 1-366 wANA

A, Residues: 1-366 wANA

A, Residues: 1-366 wANA

A, Cross-reference

C, Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.

C, Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.

C, Superfamily: vertebrate rhodopsin

C, Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; lipoprotein, F; 31-48/Domain: transmembrane #status predicted <TM1>
F; 79-96/Domain: transmembrane #status predicted <TM2>
F; 79-96/Domain: transmembrane #status predicted <TM3>
F; 107-125/Domain: transmembrane #status predicted <TM5>
F; 107-125/Domain: transmembrane #status predicted <TM5>
F; 1107-125/Domain: transmem
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                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000002A4FB; GB:X80187; GB:X80188; GB:X80189; GB:X80190 R;Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim. Biophys. Acta 1219, 171-174, 1994
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene. A;Reference number: S47529; MUID:94368850; PMID:8086459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S13638
R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor fA;Reference number: S13638; MUID:91101726; PMID:1846231
A;Accession: S13638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRHPLRARGLRSPRQAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFRSTRHN---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------FNSMRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 VIVYPSRSWEVPTNMLIALVSPLEPLSIITFCTVRIMQVLRNNEMKKFKEVQTEKKATVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWANLLVFVVCFLPLHVG--LTVRLAVG-----WNACALLETIRRALYITSKLSD----A 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 312.5; DB 28.1%; Pred. No. 2.9e-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                platelet-activating factor receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-199
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
A;Residues: 1-342 <HON>
A;Cross-treferences: UNIPROT:P21556; UNIPARC:UPI00001311BE; GB:X56736; NID:949442; PIDN:C
A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C)Accession: A54946
R; Parr, C. B.; Sullivan, D. M.; Paradiso, A. M.; Lazarowski, B. R.; Burch, L. H.; Olsen, J. C. Br.; Sullivan, D. M.; Paradiso, A. M.; Lazarowski, B. R.; Burch, L. H.; Olsen, J. C. S.; Sullivan, D. M.; Paradiso, A. M.; Lazarowski, B. R.; Burch, L. H.; Olsen, J. C. Br.; M.; Sadde, Sci. U. S. A. 91, 3275-3279, 1994
A; Reference number: A54946, MUID:94211846; PMID:8159738
A; Recession: A54946
A; Recession: A54946
A; Residues: preliminary
A; Residues: L-375 < PARs.
A; Residues: 1-375 < PARs.
A; Cross-references: UNIPARC:UPI0000145104; GB:U07225
A; Note: parts of this sequence were confirmed by protein sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPIKTAQATTRKRGIALSLVIW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
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                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-20 nucleotide receptor - human
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                      84 SDTP--LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 VVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW
                                                                                                                                                                                                                                                                                                         29 VLLIVIGLILINSLALWYFCCRM---QOWTETRIYMTNIAVADLCLICTLP--FVLHSLRDT
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                                                                                                                                                                                            Length 342;
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A;Cross-references: GDB:362713; OMIM:600041
A;Map position: 11q13.5-11q14.1
C;Superfamily: AFP receptor P2u
C;Superfamily: AFP receptor P2u
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                                                                                                                                                                                            Score 310; DB 2; I
Pred. No. 4.7e-21;
; Mismatches 110;
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                                                                                                                                                                                               Score 310;
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A57641
G protein-coupled receptor 4 - human
C; Species: Homo sapiens (man)
C; Accession: A57641
R; Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C. A; Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome A; Reference number: A57641; MUID:96129306; PMID:8595909
A; Recession: A57641; MUID:96129306; PMID:8595909
A; Recession: A57641
A; Residues: D-362 AMA>
A; Residues: J-362 AMA>
A; Residues: GDB:371710; OMIM:600551
A; Map position: J9q13.3-J9q13.3
A; Introms: #status absent
C; Superfamily: G protein-coupled receptor
C; Superfamily: G protein-coupled receptor
C; Reywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P46093; UNIPARC:UPI000016A9DF; GB:L36148; NID:g598152; PIDN:
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 RPPL-------LGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVW 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||:
171 KFPMEGWVAMMILYRVFVGFLPPWALMILSYRGILRAVRGSVST---ERQEKAKIKRLAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 ANLLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLDAICY 276
207 AVPFAVILVCYVLMARRLL-KPAYGTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINLAVADLCLLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                       266 LYYSFRSLDLSCHTLNAINMA-YKVTRLASANSCLDPVLYF 305
                                                                     239 VRLAVGW--NACALLETIRRALYITSKLSDANCCLDAICYY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 18.9%; Score 305.5; DB 2; Local Similarity 31.0%; Pred. No. 1.3e-20; Nes 93; Conservative 48; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 93,
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A;Molecule type: mRNA
A;Residues: 1-352 <MAC>
A;Cross-references: UNIPROT:P48748; UNIPARC:UP10000126ABF; EMBL:U20507; NID:g1041820; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a rabbit bradykinin B(1) recepto
                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 ANLLVFVVCFLPLHVGLTVRL----AVGWNACALLETIRRALYITSKLSDANCCLDAIC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                  RFPL------LGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVW 220
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                                                                                                                                                                                                                                                                                                                                                                                                YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 KPPMEGWVAWMNLYRVFVGPLFPWALMLLSYRGILRAVRGSVST---ERQEKAKIKRLAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCLLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C)Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S60024 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 R;MacNeil. T.; Bischilo, K.K.; Menke, J.G.; Hess, J.F.
Biochim. Biophys. Acta 1264, 223-228, 1995 A;Title: Cloning and pharmacological characterization of a rabbit bradykinii A;Reference number: S60024; MuID:96085127; PMID:7495867 A;Accession: S60024
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLIAIVLVCPAPYHVILLSRSAIYLGRPWD-CGFERVFSAYHSSLAFTSLNCVADPILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 SCSGAPDAWDLLHRL-LPTFIIAIFTLGLLGNSFVLSVFLLARRRLSVAEIYLANLAASD
                                                                                                                                                                               MINLAVADLCLLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ANLLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLDAICY
                                                                                                                                   2 NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALMVFCCRMQQWTBTRIYMTNLAVAD
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Gaps
                                                                   41;
      Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 RARGIRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTR----
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18.9%; Score 305; DB 2; Length 35;
Best Local Similarity 26.6%; Pred. No. 1.4e-20;
Matches 89; Conservative 62; Mismatches 131; Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: vertebrate rhodopsin
Keywords: G protein-coupled receptor; transmembrane protein
Query Match 18.9%; Score 305.5; DB 2; Best Local Similarity 31.0%; Pred. No. 1.3e-20; Matches 93; Conservative 48; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 YYYMAKEF------QEASALAVAPRAKAHKSQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bradykinin B1 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
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Job time : 28.5 secs

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GenCore version 5.1.7
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- protein search, using sw model OM protein

; Search time 26.5 Seconds (without alignments) 1121.924 Million cell updates/sec February 9, 2006, 00:55:13 Run on:

US-10-083-168-85 1615 1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď				
Result		Query				
No.	Score	Match	Leng	DB	ΩĪ	Description
	400	24.8	370	7	JC5549	
7	369.5	22.9	387	~	169202	G protein-coupled
e	367.5	22.8	308	~	150241	G protein-coupled
4	359.5	22.3	344	~	T09508	intron 17 purinerg
S	317	19.6	373	~	A47556	ATP receptor P2u -
9	316	19.6	362	7	833733	G protein-coupled
7	315.5	19.5	365	7	868679	G protein-coupled
60	314	19.4	328	7	I55450	G protein-coupled
Q	311.5	19.3	354	N	153033	G protein-coupled
10	311.5	19.3	362	~	A57641	
11	311.5	19.3	364	~	JQ1488	bradykinin B2 rece
12	311.5	19.3	366	Н	CORTB2	bradykinin recepto
13	309	19.1	342	N	S13638	_
14	308.5	19.1	362	~	B57641	G protein-coupled
15	307.5	19.0	362	~	S68207	G protein-coupled
16	306.5	19.0	375	N	A54946	P-2U nucleotide re
17	303	18.8	342	7	A40191	platelet-activatin
18	303	18.8		7	S60024	7
19	300.5	18.6		7	JC4162	P2Y receptor - bov
20	296.5	18.4		7	JC4737	G protein-coupled
21	292	18.1	341	7	843252	platelet-activatin
22	288	17.8		~	JC2543	angiotensin II rec
23	286.5	17.7		~	A43113	១
24	286	•	328	7	JC4800	P2Y6 receptor - hu
25	284.5	17.6		~	B45680	G protein-coupled
26	282	٠		~	863666	platelet activatin
27	280.5	•		~	S	ч
28	279.5	17.3	361	~	56	3
29	278.5	17.2	363	7	157955	somatostatin recep

somatostatin recep	angiotensin II rec	angiotensin II rec	somatostatin recep	G protein-coupled	macrophage inflamm	thrombin receptor	G protein-coupled	HHRF3 protein - hu	somatostatin recep	G protein-coupled	angiotensin II rec	G protein-coupled	somatostatin recep	somatostatin recep	somatostatin recep
JN0763	A49092	148261	I57940	S68208	I49339	151667	T09353	QQBED3	A46226	JC5067	JC2134	JC5068	A41795	C41795	A39297
N	~	N	~	0	7	~	~	-	~	~	~	~	~	~	~
364	363	363	363	365	355	420	354	323	418	355	329	369	391	391	391
		0	0	ο.	۲.	٠.	.7	S	ī,	4.	~	7	7	2.5	2.5
17.2	17.2	17.	17.	16	16	16	16	16	16	16	16	16	16	ä	Ä
278.5 17.2	277 17.2			272.5 16				267 16		264.5 16	261.5 16			261.5 16	

ALIGNMENTS

heptahelical P2Y5-like receptor - human

C;Species: Homo sapiens (man) C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004

CjAccession: UC5549
RjJanssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor. A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 cJAN>
A;Residues: 1-370 cJAN>
A;Cross-references: UNIPROT: Q99677; UNIPARC: UPI000016A4CA; DDBJ:AF005419; NID:g2240034; C;Superfamily: ATP receptor P2u

Query Match 24.8%; Score 400; DB 2; Length 370; Best Local Similarity 34.0%; Pred. No. 1.3e-29; Matches 105; Conservative 58; Mismatches 104; Indels 42;

11;

25 AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--ઠ

| |: :|||: |||: ||:||| ||: :|| ||::|||||: ||||| ::|
AVYSVVPILGLITNSVSLFVFFRFRMRARSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103 셤

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141 WVLVIGSLVARWLLGIQEGGF-----CFR-----STRHNFNSMRFPLLGFYL 182 ઠે

163 WILVLSG------GISASLFSTTNVNNATTTCFEGLSKRVWKTYLSKITIFIEVVGFII 215 쉱

183 PLAVVVFCSLKVVTALAQRPPTDVGQAEAT-RKAKRMVWANLLVFVVCFLPLHVGLTVRL 241 ઠે

g 242 AVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFORASALAVAPRAKAH 298 274 LVRSQAITNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYI-----NAH 327 ò 원

299 KSQDSLCVT 307 ò

328 IRMEŠLFKT 336

셤

RESULT 2

169202 G protein-coupled receptor HM74 - human C;Species: Homo sapiens (man) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004 C;Accession: 169202 R;Nomura, H.; Nielsen, B.W.; Matsushima, K.

10;

Gaps

43;

68 62

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intron 17 purinergic receptor P2Y5 - human
N.Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoble A;Reference number: Z16705
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNÅ
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; UNIPARC:UPI00005041B; EMBL:AF000546; NID:g2232068; E
                                                                                                                                                                                                                                                                                                        125 RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP- 176
                                                                                                                                                                                                                                                                                                                                                                                                            177 ------LIGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 STWKTYLGRIVIFIEIVGFFIPLILINVTCSTWVLRTL-NKPLTLSRNKLSKKKVLKMIFV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 FVFTLPPRIFYF-TTRNWPPGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6 TWKTYLSRIVIPIEIVGFFIPLILNVTCSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANÇCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SSHCFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDLL 65
                                                                                                                                                                                              3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVALYIFFFTLKVRNETTTYMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY
                                                                                                                                                               10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
                                                     22.8%; Score 367.5; DB 2; Length 308; 30.3%; Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%; Score 359.5; DB 2; Length Similarity 29.2%; Pred. No. 7.1e-26; Conservative 68; Mismatches 107; Indels
                                                                                                          64; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: ATP receptor reu
C;Keywords: G protein-coupled receptor; transmembrane protein
F;269-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Map position: 13
C, Superfamily: ATP receptor P2u
                                                                                                          91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 MAKEFQEA 286
                                                                              Similarity
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Best Local Si
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                A;Title: Molecular cloning of cDNAB encoding a LD78 receptor and putative leukocyte chem A;Reference number: 154751; MUID:94092629; PMID:7505609
A;Accession: 169202
A;Status: pre-innary; translated from GB/EMBL/DDBJ
A;Actus: pre-innary; translated from GB/EMBL/DDBJ
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043C3C; GB:D10923; NID:g219866; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNÅ

A,Residues: 1-308 cKAP>

A,Residues: 1-308 cKAP>

A,Residues: 1-308 cKAP>

A,Strosidues: 1-308 cKAP>

A,Cross-references: UNIPROT: P32250; UNIPARC: UPI0000055A6B; GB:L06109; NID:g304383; PIDN:
R,Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

B,ochem. alocphys. Res. Commun. 219, 105-110, 1996

A,Title: Identification of 6H1 as a PNY purinoceptor: P2N5.

A,Reference number: JC4618; MUID:96190677; PMID:8619790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:
Experimental source: T-cells
Comment: This receptor plays a role in T-cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor 6H1 - chicken
NyAlternate names: purinoceptor 6H1
C;Species: Gallus (chicken)
C;Date: 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150241; UC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: ISO241; MUID:93329058; PMID:8393036
                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSWRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 VVITALAQRPPIDVGQAEATRKAKR----MVWANLLVFVVCFLPLHVGLTVRLAVGW---- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 IIWSLRQR-----QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVL----HSLR
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                      22.9%; Score 369.5; DB 2; Length 387; 35.0%; Pred. No. 9.4e-27; tive 45; Mismatches 102; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Gene: p275
C/Superfamily: ATP receptor P2u
C/Superfamily: ATP receptor P2u
C/Superfamily: ATP receptor P2u
C/Superfamily: ATP receptor P2u
C/Superds: G protein-coupled receptor; transmembrane protein
F/15-4/Domain: transmembrane #status predicted <TM2>
F/89-109/Domain: transmembrane #status predicted <TM3>
F/133-153/Domain: transmembrane #status predicted <TM4>
F/177-201/Domain: transmembrane #status predicted <TM5>
F/177-201/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 --NACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                         C'Genetics:
A<sub>1</sub>Gens: HW14
C<sub>1</sub>Superfamily: G protein-coupled receptor 4
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 35.04 Matches 98; Conservative
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A;Residues: 1-308 <WEB>
A;Cross-references: UNIPA
A;Experimental source: T-
C;Comment: This receptor
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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43;

DB 2; Length 344;

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C;Accession: S68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expre A;Reference number: S68679; MUID:96197801; PMID:8617367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-365 <STA>
A;Cross-references: UNIPROT.P51582; UNIPARC:UPI000002E776; EMBL:X96597; NID:g1296631; PI
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 AGCLVPNLFFVTTSNKGTTVLCHDTTRPEBFDHYVHFSSAVMGLL-FGVPCLVTLVCYGL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 QEGG--FCFRSTRHNF-----NSMRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWN----ACALLETIRRALVITSK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SPLRRKSIYLVIIVLTVFAVSYLPFHVMKTLNIRARLDFQTPQMCAFNDKVYATYQVTRG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ASALAV 291
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                                                                                                                                                                                                                                                                                                                                             101 YMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLL----GI 156
                                                                                                                                                                                                                                                                                                                                                                                               44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV
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                                             ----NTCGSSDLTWPPAIKLGF-YAYLGVLLVL----GLLLNSLALWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSLPEDSSCRWAATPODSSCST 359
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Best Local Similarity 29.2%
Matches 94; Conservative
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33733
G protein-coupled receptor - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 06-Jan-1995 #text_change 09-Jul-2004
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
R; Mebb, T.E.; Simon, J; Krishek, B.J; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstochanger of the couple of the coup
                                                                                                                                                                                                                                                                                                                 Cispectes: Mus musculus (house mouse)
Cispectes: Mus musculus (house mouse)
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision: A47556
Airtitle: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
Airtitle: Expression: A47556
Airtitle: Expression: A47556
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ilarity 28.2%; Pred. No. 8.5e-22;
Conservative 63; Mismatches 134; Indels
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Best Local Similarity 30.1%
Matches 101; Conservative
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294 TSDTIQNS 301
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Best Local Similarity
Matches 96; Conserv
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G protein-coupled receptor 4 - human

G protein-coupled receptor 4 - human

G protein-coupled sapiens (man)

G; paccession: A57641

R; Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.;

Genomics 30, 84-88, 1995

A; Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome 10

A; Reference number: A57641

A; Accession: A57641

A; Accession: A57641

A; Accession: A57641

A; References: UNIPROT: P46093; UNIPARC: UPI0000050428; GB: U21051; NID: G687793; PIDN: References: UNIPARC: Constitution (C) Genetics: Constitution (C) Constitution (C)
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JHO712; A46022; A55559; JQ1488; JC1400
R;Eggerickx, D; Raspe, E; Bertrand, D; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992
A;Title: Molecular cloning, functional expression and pharmacological characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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                                                                                                                                                    YVAVRHPLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
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| : | ||:
| 171 KFPMEGWVAWMNLYRVFVGFLFPWALMLLSYRGILRAVRGSVST---BRQBKAKIKRLAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRST-RHNFNSM 173
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171 KFPMEGWVAWMNLYRVFVGFLFPWALMLLSYRGILRAVRGSVST---ERQEKAKIKRLAL
                                                                                                                                                                                                                                                                                                                               174 RFPL-------LGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 ANLLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLDAICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLIAIVLVCFAPYHVLLLSRSAIYLGRPWD-CGFBERVFSAYHSSLAFTSLNCVADPILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 RPPL------LGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
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A,Map position: 19q13.3-19q13.3
A,Introns: #status absent
C,Superfamily: G protein-coupled receptor 4
C,Keywords: G protein-coupled receptor
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94; Conservative 4
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bradykinin B2 receptor – human
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C,Superfamily: ATP receptor P2u
C,Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule Lype: DNA
A) Residues: 1-354 «RES»
A) Krestoues: 1-354 «RES»
A) Krestoues: UNIPROT: P46093; UNIPARC: UP1000016A9DF; GB:L36148; NID:G598152; PIDN:
C; Superfamily: G protein-coupled receptor
C; Keywords: G protein-coupled receptor
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CiSpecies: Homo sapiens (man)
CiDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CiDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
CiAccession: 15303
RiHeiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, DNA Cell Biol. 14, 25-35, 1995
A;Title: Isolation of three novel human genes encoding G protein-coupled receptors.
A;Reference number: 153033; MUID:9513435; PMID:7832990
G protein-coupled P2 receptor - rat
G protein-coupled P2 receptor - rat
G protein-coupled P2 receptor - rat
Cipate: 02-Unl-1996 #sequence_revision 02-Unl-1996 #text_change 09-Unl-2004
Cipate: 02-Unl-1996 #text_change 09-Unl-2004
AiReference number: 155450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTAIAVDRYVAVRHPLRARGLRSPRQAA-AVCAVLWVLVIGSLVARWLL---GIQEG-GF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
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19.3%; Score 311.5; DB 2; Length 354;
Best Local Similarity 31.3%; Pred. No. 2.2e-21;
Matches 94; Conservative 48; Mismatches 117; Indels 41;
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LDPILFYFTQQKFR 309
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Best Local Similarity 30.3%
Matches 95; Conservative
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A; Molecule type: mRNA
A; Residues: 1-366 <MCE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-366 < WAN>
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A;Molecule type: DNA
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A; Residues: 1-364 < MAA>
A; Cross-references: UNIPARC: UPI000002A4FC; GB:L27594
R; Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Bjochem. Biophys. Res. Commun. 184, 260-268, 1995
A; Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) recept A; Reference number: JQ1488; MUID:92231936; PMID:1314587
A; Accession: JQ1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: GDB:BDKRB2
A;Gene: GDB:BDKRB2
A;Gene: GDB:BJKRB2
A;Gene: GDB:BJKRB2
A;Gross-references: GDB:135713; OMIM:113503
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;34-56/Domain: transmembrane #status predicted <TM2>
F;66-92/Domain: transmembrane #status predicted <TM2>
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A;Residues: 1-164 «HES>
A;Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID
A,Reference number: JH0712; MUID:93038601; PMID:1329734
A,Accession: JH0712
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1.364 < EGGS
A,GROSS-references: UNIPROT:P30411; UNIPARC:UPI000002A4FC; GB:S45489; NID:9256536; PIDN:
R,Powell, S.J.; Slynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.
Genomics 15, 435-438, 1993
A,Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to ch
A,Reference number: A46022; MUID:93194199; PMID:7916737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 LVSIDRYLALVKTMSMGRMRGVRWAKLYSLVIWGCTLLLSSPMLVFRTMKEYSDEG---- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |:| :| ||:|::|::|| |::|::|| CDERRATVIVIVIVILLIFIICWLEPROISTFIDTLHRIGI-LSSCODERIIDVITOIASFMA 294
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Filo4-127/Domain: transmembrane #status predicted <TW4>
Filo4-127/Domain: transmembrane #status predicted <TW4>
Filo5-221/Domain: transmembrane #status predicted <TW6>
Fi20-1266/Domain: transmembrane #status predicted <TW6>
Fi20-1266/Domain: transmembrane #status predicted <TW7>
Fi20-121/B0/Binding site: carbohydrate (Asn) (covalent) #status predicted Fi10,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
Fi20-121/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
Fi20-121/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status
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Matches 89; Conservative
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A;Molecule type: DNA
A;Residues: 1-364 <POW>
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bradykinin receptor type B-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283; A55079; B47529
R;McBachern, A.E.; Shelton, E.R.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppan, P.; Fujis Proc. Natl. Acad. Scl. US.A. 88, 7724-7728, 1304
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
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C; Superfamily: vertebrate rhodopsin
C; Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein, F; 31-48/Domain: transmembrane #status predicted <TM1>
F; 79-96/Domain: transmembrane #status predicted <TM3>
F; 19-710/Domain: transmembrane #status predicted <TM4>
F; 19-710/Domain: transmembrane #status predicted <TM4>
F; 19-710/Domain: transmembrane #status predicted <TM6>
F; 19-7215/Domain: transmembrane #status predicted <TM6>
F; 19-7216/Domain: transmembrane #status predicted <TM7>
F; 19-7216/Domain: transmembrane #status predicted <TM7
F; 19-7216/Domain: transmembrane #s
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Biochim. Biophys. Acta 1219, 171-174, 1994
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.
A;Reference number: S47529; MUID:94168850; PMID:8086459
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A; Cross-references: UNIPROT: P25023; UNIPARC: UPI00001708A1; GB:M: Bader, M. B; Biol. Chem. 269, 26920-26925, 1994
A; Title: Molecular structure and expression of rat bradykinin B2 receptor gene
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295 YSNSCLNPLVYVIVGKRFRKKS 316
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28.1%; Pre-
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completed: February 9, 2006, 01:01:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 AICY 276
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossidues: 1-342 <HON>
A;Cross-references: UNIPROT: P21556; UNIPARC: UPI00001311EE; GB:X56736; NID: 949442; PIDN: CA;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                C; Species: Cavia porcellus (guinea pig)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: S13638
R; Honda, 2.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To Nature 349, 342-346, 1991
A; Title: Cloning by functional expression of platelet-activating factor receptor from gu A; Reference number: S13638; MUID: 91101726; PMID: 1846231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BESULT 14
B5761

B5761

B5761

C;Date: Coupled receptor 4 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: O8-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Date: O8-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: B57641
R;Mahadevan, M.S; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.Genomics 30, 84-88, 1995
A;Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome A;Reference number: A57641; MUID:96129306; PMID:8595909
A;Accession: B57641
A;Accession: B57641
A;Accession: Landarinary; nucleic acid sequence not shown; translation not shown; signification A;Residues: 1-362 <MAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLVIGSLVARWILGIQE-----GGFCFRSTRHNFNSMRFPL-----LGFYLPLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 VVVPCSLKVVTALAQRPPIDVGQAEATRKAKRWWANLLVFVVCFLPLHVGLTVRLAVGW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 LILFCNLVIIHTLLRQPVKQQRNAEVRRRALMMVCTVLAVFVICFVPHHM-----VQLPW 255
247 VLAVLGLFVLCWFPFQISTFLDTLLRLGVLSGCWN------ERAVDIVTQISSYVAYS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 IIFVLGIIANGYVLWVP-ARLYPSKKLNBIKIFWVNLTVADLLPLITLPLMIVYSYSNQGN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 SDTP--LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 VLLVIGLLINSLALWVFCCRM---QQWTETRIYMTNLAVADLCLLCTLP--FVLHSLRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 TLABLGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 NACAL-----LETIRRALYITSKLSDANCCLDAICYYYMAKEFQE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.1%; Score 309; DB 2; Length 342; 28.2%; Pred. No. 3.6e-21; cive 58; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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19.1%; Score 308.5; DB 2;
Best Local Similarity 30.6%; Pred. No. 4.3e-21;
Matches 93; Conservative 48; Mismatches 114;
                                                                                                                                                                                                          platelet-activating factor receptor - guinea pig
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                                                                                         299 NSCLNPLVYVIVGKRFRKKS 318
                                           268 NCCLDAICYYYMAKEPQEAS 287
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Best Local Similarity 28.2*
Matches 81; Conservative
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G protein-coupled receptor 6C.1 - human
C.Species: Homo aspiens (man)
C.Species: Homo aspiens
R.Species: Second (man)
R.Sp. 121-124, 1995
R.Species: J.Sp. 121-124, 1995
A.Stelses: Coning, sequencing and tissue distribution of two related G protein-coupled rec
A.Reference number: S68207; MUID:96087098; PMID:7498459
A.Stelses: S68207
A.Stelses: Man,
A.Stelses: Man,
A.Stelses: Mulphort: P46093; UNIPARC:UPI000016A24A; EMBL:U35399; NID:glo15420; PIII
C.Superfamily: G protein-coupled receptor
C.Superfamily: G protein-coupled receptor
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                                                                                                                                                                                                                                          YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGS----LVARWLLGIQEGGFCFRST-RHN 169
                                                                                                                                                                                                                                                                                                                                                                                                         174 RFPL-------LGFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAKRNVW 220
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                               3 NGTWEGCHVDSRVDHLFPPSL-----YIFVIGV-GLPTWCLRLWAAYRQVRQKRNELGYY
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171 KPPMBGWVAWMNLYRVFVGFLFPWALMLLSYRGILRAVRGSVST---BRQEKAKIKRLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 MINLAVADLCLLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR
                                                                                                                                                                                                                                                                                                                                                                   170 FNSMRPPL------LGFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 RMVWANILLVFVVCFLPLHVGLTVRLAV----GWNACALLETIRRALYITSKLSDANCCLD
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NGTYNTC---GSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIY
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19.0%; Score 307.5; DB 2;
Best Local Similarity 31.0%; Pred. No. 5.3e-21;
Matches 93; Conservative 49; Mismatches 117;
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                                                                                                                                         9, 2006, 00:47:43; Search time 165 Seconds (without alignments) 1321.262 Million cell updates/sec
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                                                                                                                                                                                                                                                                1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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06zmp9
04vbb5
09vebb5
09vebb6
09cb97
08bcb97
08bcb97
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Q9wu09
P43657
Q9h1c0
Q5ku18
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                     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                                                                                                                                      2166443 segs, 705528306 residues
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Q4ZPY2 HUMAN

Q4ZPY2 HUMAN

Q4YBN5 HUMAN

Q8ZBV3 MOUSE

Q5ZU3 HUMAN

Q5BUS9 MOUSE

Q4BUX1 MOUSE

Q4BUX1 MOUSE

Q4BUX1 MOUSE

Q4BUX2 HUMAN

G8BX5 HUMAN

G8R55 HUMAN

Q8RCE4 HUMAN

Q8RCE4 HUMAN

Q8RCE4 HUMAN

Q8RCE4 HUMAN

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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                                                                                                                                                Run on:
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61 NLAVADLCLLCTLPFVLHSLRDTSDTFLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH 120
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                                  homo sapien
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xenopus lae
homo sapien
sus scrofa
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                                                                            xenopus tro
                                                                                               rattus norv
homo sapien
          rattus norv
mus musculu
                                                                                       mus musculu
                          rattus norv
                                                                                                               sus scrofa
                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIYMT
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Last sequence update)
Last annotation update)
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Pred. No. 7.1e-112;
0; Mismatches 2;
                                                                                                                                                                                      309 AA
                080E54_MOUSE
P2RY2_RAT
P2RY2_HUMAN
Q40EN1_HUMAN
G5KGS6_XENLA
GPR81_HUMAN
CLIR2_PIG
G6P852_XENTR
GPR81_MOUSE
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7 HUMAN
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QEFHIS;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
  [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
  NCBI_TaxID=9606;
                                                                                                                                                                                                                                    GPR35 protein.
Name=GPR35;
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Matches 307;
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YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRMVWANLLVFVVCFLPLHVGLTVR

PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180

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61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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 Pfam, PF00001; 7tm 1; 1.

PROMING, PRO0237; GFCRRHDODEN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Transducin coupled receptor; Glycoprotein; Polymorphism; Receptor; Transmembrane.

TOPO_DOM

TOPO_DOM

TOPO_DOM
                                                                                                                                                                                                                                                         7 (Potential).
Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1597; DB 1; Length 309;
Pred. No. 2e-111;
0; Mismatches 3; Indels
                                                                                            1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential)
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/FTId=VAR_013606.
A -> R (in Ref. 1).
97734FB7231B26F0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             FTId=VAR_013603
                                                                                                                                                                                                                                                                                                                                                                                                     FTIG=VAR_013604
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/FTId=VAR 013605.
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Q4ZFV2;
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13-SEP-2005 (TrEMBLrel. 31,
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309 AA;
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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                       241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM, 602646; -. Goldegral to plasma membrane, TAS. GO; 0005887; C:integral to plasma membrane, TAS. GO; 00:0004930; F:G-protein coupled receptor activity, TAS. GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND MED-183.
MEDLINE-20472315; PubMed=11017071; DOI=10.1038/79876;
MEDLINE-20472315; PubMed=11017071; DOI=10.1038/79876;
Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hincklo Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
Honofto Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus.";
Net. Genet. 26:163-175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE, AND VARIANT ARG-294.
MEDLINE-98140132; PLUMEd-9479505; DOI=10.1006/geno.1998.5095; O'Dowd B.P., Nguyen T., Marchese A., Cheng R., Lynch K.R., Heng H.H.Q., Kolakowski L.F. Jr., George S.R.; "Discovery of three novel G-protein-coupled receptor genes.",
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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                TISSUE=Brain:

Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Kawakami B., Sugiyama A., Takemoto M., Ishii S., Yamamoto J.,

Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,

Yamashita H., Mareuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Magateuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,

Submitted (MAR-2004) to the EMBL/GenBank/DubJ databases.

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL; AK131540; BAD18676.1; -; mRNA.

EMBL; AK131540; BAD18676.1; -; mRNA.

Roj. Go:0001681; C:integral to membrane; IEA.

GO; GO:001581; F:receptor activity; IEA.

ROj. Go:000186; P:receptor activity; IEA.

ROj. GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

InterProf. IPROGONO76; GPCR. Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 MNGTYNTCGSSDLTWPPAIKLGFYAXLGVLVLGLLINSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSNAFPLLGF
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                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR0001; 7tm i, 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G-ROTEIN RECEP_F1_1; 1.

PROSITE; PS0262; G-PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 394 AA; 43309 MW; 1598FD44BAB4233C CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
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Hypothetical protein FLJ16773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4VBNS_HUMAN PRELIMINARY;
Q4VBNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPR35 protein (Fragment).
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                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                               NCBI_TaxID=9606;
                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=GPR35;
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                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
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                                                                                                                                                                                                                                                                             Haakenson W., Trani L., Schatzkamer K.; "The sequence of Homo sapiens BAC clone RP11-27M15."; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.H.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA; 34072 MW; 97734FB7231B26F0 CRC64;
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Last annotation update)
     Last annotation update)
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Q6ZMP9;
05-JUL-2004 (TYEMBLRE1: 27,
05-JUL-2004 (TYEMBLRE1: 27,
05-JUL-2004 (TYEMBLRE1: 27,
                       Hypothetical protein GPR35
Name=GPR35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
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     13-SEP-2005 (TrEMBLrel.
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Submitted (OCT-2002)
                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transducer;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-22388257; PubMed=12., Shemmen C.M., Schuler G.D.,
WEDLINE R.P., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
WEDLINE-2248 M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
WEDLINE S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
WEDLINE S.A., McEwan P.J., McKernan K.J., Male M.A., Gay L.J., Hulyk S.W.,
WILALON D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulton R., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Wenting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Wenterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Wenterfield Y.S.N., Wenterfield M.A., Johnson M.A.,
Wenterfield Y.S.N., Well Janalysis of more than 15,000 full-length human
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

EMBL: BC095500; AHPS500.1; -; mRNA.

InterPro; IPR000276; GPCR_Rhodpsn.

PRINTS; PR00237; GPCRRHODPSN.

PROSITE; P600237; GPCRRHODPSN.

PROSITE; P600237; GPCRRHODPSN.

GPCRRHODPSN.

G-protein coupled receptor; Receptor; Transmembrane.
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308 AA; 33941 MW; 5791BF9CR7206034 CRC64;
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99.0%; Pred. No. 4.7e-111;
iive 0; Mismatches 3;
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NIH MGC Project;
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Matches 305; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences.
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                                    NCBI_TaxID=9606;
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SEQUENCE
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MEDINE-2578L/657, TISSUE-ANDMAN GRAND GRAN
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                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genetic variation in the gene encoding calpain-10 is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
--- FUNCTION: Orphan receptor.
--- SUBCELLUIA: LOCATION: Integral membrane protein (By similarity)
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
MEDLINE=20472315; PubMed=11017071; Li X., Orho-Melander M., Hara M., Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
del Bosque-Plate L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable G-protein coupled receptor 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF200349; AAG18487.1; -; mRNA.
EMBL; BC027429; AAB77429.1; -; mRNA.
ERSembl; ENSWUSG0000002621; Mus musculus.
MGI; MGI:1929509; Gpr35.
GO; GO:0016021; C:Intregral to membrane; TAS.
InterPro; IPR000276; GPCR, Rhodpsn.
InterPro; IPR0002286; P2_purnocptor.
   307 AA
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PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01157; P2YPURNOCPTR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type 2 diabetes mellitus.";
Nat. Genet. 26:163-175(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
   STANDARD;
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
GPR35_MOUSE
                                                                                                                                                                              Name=Gpr35;
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Query Match
Best Local Simil
Matches 223;
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                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                       MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                       Gaps
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Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Probable G-protein coupled receptor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLUTAR LOCATION: Integral membrane protein (By similarity).
-1- SUMILARITY: Belongs to the G-protein coupled receptor I family.
EMBL; AB041940; BADB3594.1; -; mRNA.
                                                                                                                                  Cytoplasmic (Potential).

N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
By similarity.
Glycoprotein; Receptor; Transducer;
                                                                                                                                                                                                       ;
9
                                                                                                                                                                                    Length 307;
                                                                                                                                                                                                      51; Indels
                                                        3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                        6 (Potential).
Extracellular (Potential)
7 (Potential).
                                                Extracellular (Potential)
                                                                                                                                                                     0B3D02CECB16710D CRC64;
                Extracellular (Potential)
                                                                                          5 (Potential).
Cytoplasmic (Potential).
                                Cytoplasmic (Potential) 2 (Potential).
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Last annotation update)
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;; Pred. No. 5.3e-76;
30; Mismatches 51;
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                                                                                                                                                                      34152 MW;
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 receptor;
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Name=KPG 007;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSKU21_HUMAN PRELIMINARY;
                                                                                                                                                                                            Local Similaricy
hes 223; Conservative
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KSQDSQILSL 306
                87
307 AA;
G-protein coupled
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        Transmembrane
TOPO_DOM
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CARBOHYD
DISULFID
SEQUENCE
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TOPO DOM
TRANSMEM
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TOPO_DOM
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GEYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLT 238
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                                                                                                                   Transmembrane
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0045028; F:purinergic nucleotide receptor activity, G-.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004884; F:receptor activity; IEA.
GO; GO:0001884; F:redopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0007186; P:gignal transduction; IEA.
InterPro; IPR002286; P2_purnocptor.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male bone cDNA, RIKEN full-length enz
clone:9830121M19 product:G protein-coupled receptor 35,
                                                                                                                                                                                                                                                                                                                                                                                                          Length
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PRINTS; PR00237; GPCRHODOPRN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

PROSITE; PS00262; G PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transducer; Trans

SEQUENCE 307 AA; 34152 MW; 0B3D02CECB16710D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          69.5%; Score 1123; DB 2; 71.9%; Pred. No. 5.3e-76; iive 30; Mismatches 51;
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Q8CB97;
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KSQDSQILSL 306
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A MARINE W. HURTA N. PHUNISH N. KUCHON H. Addell J. Noble S. WARRANG T. SHIPE N. MARINE W. TISHER W. PIRIN K. RIJOHNEN H. KOOD S. CREWARK T. SHIPE N. MARINE M. MARINE M. MARINE M. MARINE M. CORPER N. MARINE M. MARINE M. CORPER N. MARINE M. MARINE
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TISSUE-Embryonic body between diaphragm region and neck;

TISSUE-Embryonic body between diaphragm region and neck;

MEDLINE-21086660; PubMed=11217851; DOI=10.1038/35055500;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QERSOB MOUSE PRELIMINARY; PRT; 307 AA.
(085296)
10-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430051L15 product:G protein-coupled receptor 35, full insert sequence.
                                                                                                                                                            Transducer; Transmembrane
                                                                                                                                                                                                                                                                                                                                                . 9
                                                                                                                                                                                                                                                                  Query Match 69.5%; Score 1122; DB 2; Length 307; Best Local Similarity 71.9%; Pred. No. 6.2e-76; Matches 223; Conservative 30; Mismatches 51; Indels
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Trans SEQUENCE 307 AA; 34140 MM; 8BB439AAED5F7656 CRC64;
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TISSUB-Embryonic body between diaphragm region and neck;
TISSUB-Embryonic body between diaphragm region and neck;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Hayashida K., Hayatsu N., Hirancko K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakaura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
A sato R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

I. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AKO18480; BAC28861.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J;

C TISSUB=Embryonic body between diaphragm region and neck;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Itoh M., Aizawa J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Asumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tarawa M., Ohara B., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y:, Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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MEDINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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prepare full-length cDNA libraries for rapid discovery of new genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                  IISSUE=Embryonic body between diaphragm region and neck; The FANTOM Consortium,
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PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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GO; GO:0016021; C:integral to membrane;
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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                                                                                                                                                                                     61 NLAVADICILCTLPFVLHSLR-DISDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                             179 GFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLT
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Genoscope, Whitehead Institute Centre for Genome Research;
Genoscope, Whitehead Institute Centre for Genome Reseas.
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Chromosome I CAF7335, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00004207001,
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodon.
                 Transmembrane.
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                                                                           tch 68.6%; Score 1108; DB 2; Length 307; al Similarity 71.3%; Pred. No. 6.9e-75; 221; Conservative 30; Mismatches 53; Indels
                 G-protein coupled receptor; Receptor; Transducer; TransEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Nature 431:946-957(2004).
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                                                                                  Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Peingold R.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Pahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 RHNFNS---MRPPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVMANL
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-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. Bable, CARSO110735; CAF90112.1, -; Genomic_DNA. InterPro, IPR000276; GPGR Rhadpsn. InterPro, IPR002188; P2Y5_purnocptor.
                                                                                        Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01067; PZYSORPHARR.

PROSITE; P800237; G PROTEIN RECEP F1 1; 1.

PROSITE; P850262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                             25.8%; Score 416.5; DB 2; Length 305; 34.6%; Pred. No. 3.38-23; Artive 59; Mismatches 108; Indels 33
                                                                                                                                                                                                                                                                305 AA; 34283 MW; E9F740AD3FF04F32 CRC64;
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Q502U9;
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NUCLEOTIDE SEQUENCE
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ESFQKS 304
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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13-SEP-2005
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                             Query Match
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44 AVSVVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLFFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 WPPGDT-LCKISGTAPLTNIYGSMLPLTCISVDRPLAIVYPPRSRIKTRRNSAIVCAGY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVLVIGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : :| || : || || : || |281 TNCFLERFAKIMYPITLCLATINCCPDPFIYYPTLESFQKSFYI-----NAHIRMESLF 334
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AYLGVILVIGILINSLALWVFCCRMQOWTETRIYMTNLAVADLCILCTLPF-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL: BC095538; AAB95538.1; -j. mRNA.
ERBembl; ENSG00000147145; Homo sapiens.
InterPro; IPR001276; GPCR Rhodpsn.
InterPro; IPR02188; P2Y5 purnocptor.
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MEDLINE=97225799; PubMed=9073069; DOI=10.1016/80378-1119(96)00722-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS0023', G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262, G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41881 MW; 38267561B1029848 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
P2Y purinoceptor 9 (P2Y9) (Purinergic receptor 9)
receptor GPR23) (P2Y5-like receptor).
                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 402; DB 2; 34.1%; Pred. No. 4.7e-22;
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                                                                                                                                                                                                                                                                                                                                             TISSUE=G-protein coupled receptors;
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PRINTS; PR01067; P2Y5ORPHANR.
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Homo sapiens (Human).
                                                                                                                                                                                      and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE.
MEDLINE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
MADLINE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
MADLINE=97366061; Doing of a human heptahelical receptor closely related to the P2Y5
O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H. Kolakowski L.P. Jr., Lynch K.R., George S.R.; Theng H.H. "Cloning and chromosomal mapping of four putative novel human G-protein-coupled receptor genes."; Gene 187:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopatz S.A., Aronstam R.S., Sharma S.V.; incDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 236:106-112(1997).
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                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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Krausbes-Eralli,

MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

R trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R tlauener R.D., Colline F.S., Wagner L., Shamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul R.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R schaefer M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robark S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Martaffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Martaffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Martaffield W.S., Wonener B.J., Marra M.A.;

Rodereztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; TAS.
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-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUB SPECIFICITY: Not detected in the brain regions thalamus,
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GO:0004930; F:G-protein coupled receptor activity; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR0167; P2YSORPHANR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A., Lehrach H., Meindl A., Minx P. J., Hillier L.W., Willard H.F., Walson R. K., Materston R. H., Rice C.M., Vaudin M., Coulson A., Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T. Gibbs R.A., Beck S., Rogers J., Bentley D.R.; "The DNA sequence of the human X chromosome."; Nature 434:325-337(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putamen, caudate, frontal cortex, pons, hypothalamus and
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
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AY301274; AAP58404.1; -; Genomic_DNA.
AL590083; CAD18851.1; -; Genomic_DNA.
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EMBL; U90323; AAB62087.1; -; Genomic_DNA.
EMBL; U90322; AAB62088.1; -; mRNA.
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HGNC; HGNC:4478; GPR23.
                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR002188; P2Y5_purnocptor.
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BC074722; AAH74722.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
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EMBL;
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NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
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Matches 103; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                         Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

7 (Potential).

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Pot 
                                          4 (Pocential).
Extracellular (Potential)
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     Cytoplasmic (Potential).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TremBLrel. 27, Last annotation update)
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P -> L (in Ref. 3)
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     Homo sapiens (Human)
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NUCLEOTIDE SEQUENCE
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University Register, Course;

A birector MGC Project;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

L Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

R G-1 SubCELLIAR LOCATION: Integral to membrane; IRA.

RG-1 GO:00016021; C:integral to membrane; IRA.

RG-1 GO:00016021; C:integral to membrane; IRA.

RG-1 GO:00016021; C:integral to membrane; IRA.

RG-1 GO:0001803; F:receptor activity; IRA.

RG-1 GO:000186; F:receptor activity; IRA.

RRINTS; PR00021; GPRCRHONPR.

RRINTS; PR00021; GPRCRHONPR.

RRINTS; PR001601; 74m.

RRINTS; RROSCAP; GPRCREIN RECEPTI; UNKNOWN.

RRINTS; RROSCAP; GPRCREIN RRCREP FI. 2; 1.

RROSTER; PS50262; G PROTEIN RECEPTOR; Transdmenbrane.

SQ SEQUENCE 370 AA; 41867 MW; 2AB48B75F43FFF83 CRC64;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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QBEKKI;
QBEKKI;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:D130067B12 product:P2Y PURINOCEPTOR 9, full
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Azawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Azawa K., Masuda H., Ashburnar M., Batalov S., Casavant T.,
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Rh Kuchl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
Rh Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagnar L., Washio T.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Nasaki Y., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/61; TISSUE=Spinal ganglion;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Spinal ganglion; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Maramatsu M., Hayashizaki Y.; Shibata I., Okazaki Y., Maramatsu M., Hayashizaki Y.; Shibata Bubtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                     Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                               STRAIN=C57BL/67; TISSUE=Spinal ganglion; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 420:563-573 (2002)
                                                                             Murinae; Mus.
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                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                            NCBI_TaxID=10090;
                                                                                                                                   NUCLEOTIDE
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226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 VVCFLPLHVGLTVRLAVGWNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AVADLCLLCTLPF-VLHSLR---DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI; MGI:1925384; Gpr23.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:G-profein coupled receptor protein signalin. .; IEA.

GO; GO:0007186; P:signal transduction; IEA.

InterPro; IPR00276; GPCR_Rhodopsn.

InterPro; IPR002188; P2YS_purnocptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 VVCFVPYNSVLFLYALVRSQAITNCLLERFAKIMYPITLCLATLNCGFDPFIXYFTLESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TYNTCGSSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNL
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Gaps
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
enriched library, clone:Bl30055Ll5 product:P2Y PURINOCEPTOR 9, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01067; P2Y5ORPHANR.
PROSITE; PS010537; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 370;
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24.7%; Score 399; DB 2; Length 37
Best Local Similarity 34.3%; Pred. No. 7.9e-22;
Matches 104; Conservative 59; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001; 7tm 1; 1
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ID QBEIGZ M
ORBIGZ M
ORBEIGZ M
OI - MAR - 20
DT 01 - MAR - 20
DF 02 - MAR - 20
DF 03 - MAR - 20
DF 04 - MAR - 20
DF 04 - MAR - 20
DF 05 - MAR - 20
DF 06 - MAR - 20
DF 07 - MAR - 2
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                                                                                                                                                                                          STRAIN-CSTBL/631 TISSUE-Parthenogenote;

KREDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

KREDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arawaw T., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

A Arawaw K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Pleischmann W., Gasateriand T., Gissi C., King B., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F.,

Burnhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashia-sahi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE.
STRAIM-C57B1/61; TISSUG-Parthenogenote;
STRAIM-C57B1/61; TISSUG-Parthenogenote;
MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; PubMed-11078 K., Niteunal T., Tashiro H., Itoh M., Shibara T., Nishiro H., Itoh M., Shonnoto R., Maramaca A., Nishiro T., Harada A., Pujiwake S., Inoue K., Togawa K., Tanaka T., Natsuura S., Marahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Norazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Kawai T., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Parthenogenote;
The PANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
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                                                      STRAIN=CS7BL/6J; TISSUE=Parthenogenote;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-langth cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katich M., Kouda M., Nomura K., Mutaka M., Ohsato N., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                  [1] _
NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
WCBI_TaxID=10090;
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104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLALVYPFRSRTIFTRRNSALVCAGY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AVSVVFILGLITSSASLFVFCFRMKMRSETAIFITNLALSDLLFVCTLPFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSLKVVTALAQRPPTDVGQAEAT-RKAKRMVMANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                                                                                                                                                                   Ensembl; ENSMUSGRO000049929; Mis musculus.

MGI; MGI:1925384; Gpr23.

GO; GO:0016021; C:integral to membrane; IRA.

GO; GO:0016021; F:purinergic nucleotide receptor activity, G-. . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000186; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007185; F:rhodopsin-like receptor in signalin. .; IEA.

GO; GO:0007185; P:signal transduction; IEA.

InterPro; IRR000205; GPR Rhodopsn.

InterPro; IRR000205; GPR Rhodopsn.

InterPro; IRR0002186; P2Y5_purnocptor.
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saaki D., Shibata K., Shinaqawa A., Shiraki T., Sogabe Y., Tagami M. Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T. Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (UTL-2001) to the RMBI/GenBank/DDBJ databases.

-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL, AKO45289; BAG32299.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AYLGVILVIGILINSLALWVPCCRMQQWTBTRIYMTNIAVADLCLLCTLPP-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIGHTS, PROCEST, GPECRHODOPSN.
PRINTS, PRO1067; P2YSORPHANR.
PROSITE, PSO037; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PSS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41872 MW; 084C79FEDF032050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.2%; Score 391; DB 2; Length 37 34.5%; Pred. No. 3.1e-21; ive 59; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 TNCLLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 34.5:
tes 97; Conservative
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Matches
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Search completed: February 9, 2006, 01:00:18 Job time : 166.5 secs us-10-083-168-85.rai

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February 9, 2006, 01:00:39; Search time 33.5 Seconds (without alignments) 762.591 Million cell updates/sec
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1615
1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/HCOMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	20	2, A	15	36,	222,	108,	21,	135,	œ`	ω,	4, 4	30,	30, A	137,	157,	13	83	17	Э, А	24	88,	18, 7	374,	12	(1	46	Sequence 2, Appli
SUMMARIES	ΩI	US-09-422-869-20	US-08-781-250-2	US-10-314-048A-159	US-10-314-048A-36	US-09-170-496D-222	US-09-170-496D-108	US-09-944-807-21	US-10-314-048A-135	US-08-467-948A-8	US-08-467-947A-8	US-09-875-076-4	US-08-467-948A-30	US-08-467-947A-30	US-10-314-048A-137	US-10-314-048A-157	US-10-314-048A-139	US-09-964-956-83	US-09-745-842-17	US-09-102-710B-3	US-10-314-048A-24	US-10-314-048A-88	US-09-979-603-18	US-08-513-974B-374	US-10-314-048A-151	US-09-585-876-2	-09-826-209-	US-09-979-603-2
	DB	~	7	7	~	N	N	~	~	-	N	7	н	~	~	N	~	~	~	~	~	N	N	~	~	~	~	7
	Query Match Length DB	309	370	363	363	387	387	387	387	344	344	372	302	302	360	351	361	254	377	374	346	346	345	362	343	346	391	346
do	Query	9.66	24.8	23.7	23.3	23.2	22.9	22.9	22.9	22.3	22.3	22.3	22.3	22.3	21.6	21.1	21.1	20.4	20.3	20.3	20.3	20.0	19.9	19.8	19.8	19.7	19.7	19.6
	Score	1609	401	382.5	376.5	374.5	369.5	369.5	369.5	360.5	360.5	360	359.5	359.5	348.5	340.5	340	329.5	328.5	327.5	326	323.5	321.5	320	319.5	318.5	317.5	316.5
	Result No.	-1	8	e	47	ß	ø	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 14, Appl Sequence 22, Appl Sequence 15, Appl Sequence 16, Appl Sequence 2, Appli Sequence 60, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 166, App Sequence 255, App Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
US-10-314-048A-14 US-09-979-603-22 US-09-745-842-15 US-09-745-842-16 US-09-077-173D-2 US-09-077-173D-2 US-09-170-496D-4 US-09-170-496D-186 US-09-170-496D-186 US-09-170-496D-186 US-09-170-496D-186 US-09-170-496D-186 US-09-170-496D-186 US-09-170-496D-166 US-09-442-134A-2 US-08-442-134A-2 US-08-444-581B-2 US-08-444-681B-2 US-08-444-6088A-2 US-08-446-088A-2
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316.5 316.3 316.3 316.3 315.5 311.5 311.5 311.5 311.5 310.0 310.0 30.0 30.0 30.0 30.0 30.0 30
2 2 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

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APPLICANT: Benan, Dominic F.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: 6.02 the Treatment of Metabolic-Related Disorders
FILE REPERENCE: 22.036.CIP
CURRENT FILING DATE: 20.02-12-06
PRIOR PILING DATE: 2002-03-12
PRIOR PLICATION NUMBER: 09/995,543
PRIOR PLICATION NUMBER: 60/399,917
PRIOR PLICATION NUMBER: 60/399,917
PRIOR PLING DATE: 2002-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEPQEASALAVAPRAKAHKSQDSLC 305
                                                                                          | ::||| ::||| ::||| | ::||| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 159, Application US/10314048A Patent No. 6902902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Connolly, Daniel
APPLICANT: Choi Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lowitz, Kevin P.
Behan, Dominic P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi, Bryan
Leonard, James
Hakak, Yaron
Liaw, Chen
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Best Local S:
Matches 97
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Stephanie
APPLICANT: Van Horn, Stephanie
APPLICANT: Bag, Derk
APPLICANT: Mag, Derk
APPLICANT: Mag, Derk
APPLICANT: PA
STATE: PA
CUNTRY: UGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AVSVVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLFFKIFYNFNRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
FILING DATE: 10-JAN-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY,AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATG50043
                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08781250 Patent No. 6010877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: William T. Han,
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATC
TELECOMMUNICATION INPOSNATION:
TELEPHONE: 610-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%;
Best Local Similarity 34.1%;
Matches 103; Conservative 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Distriction
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: Human G Protein-Coupled Receptors
TITLE OF INVENTION: Human G Protein-Coupled Receptors
TITLE OF INVENTION: Human G Protein-Coupled Receptors
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT APPLICATION NUMBER: 10/096,511
PRIOR PILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-03-99,917
PRIOR PILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
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264 QNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
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                                                                                         Sequence 36, Application US/10314048A; Patent No. 6902902; GENERAL INFORMATION:
                                                                                                                                                                                            Richman, Jeremy
Connolly, Daniel
                                                                                                                                                                                                                                                                       Leonard, James
Hakak, Yaron
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97; Conservative
                                                                                                                                                   Unett, David J.
Chen, Ruoping
                                                                                                                                                                                                                                  Dang, Huong T.
Choi, Bryan
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Best Local (
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APPLICANT:
APPLICANT:
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Sequence 222, Application US/09170496D Patent No. 6555339

RESULT 5 US-09-170-496D-222

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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-CTITLE OP INVENTION: Receptors
FILE REPERBNCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 222
LENGTH: 387
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOOTWARE: Patentin Version 3.1
SEQ ID NO 108
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                                                                                                                                                                                                                                                                                                                                                                            ;; Score 374.5; DB 2;
;; Pred. No. 1e-24;
47; Mismatches 107;
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; Patent No. 6555339
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Best Local Similarity 34.4%;
Matches 95; Conservative 4'
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US-09-170-496D-108
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE REPRENCE: 22.USG.CIP
FILE REPRENCE: 22.USG.CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR PLICATION NUMBER: 05/395,543
PRIOR PLICATION NUMBER: 06/399,917
PRIOR PLICATION NUMBER: 60/399,917
PRIOR PLICATION NUMBER: 60/404,761
PRIOR PLICATION NUMBER: 60/404,761
PRIOR PLICATION NUMBER: 60/410,747
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APPLICANT: CAO, LIANG
APPLICANT: GENTZ: REINER
APPLICANT: GENTZ: REINER
APPLICANT: GENTZ: REINER
APPLICANT: BULT, CAROL J.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GFRZ
NUMBER OF SEGUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE
STREAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 387;
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1 Similarity 35.0%; Pred. No. 2.7e-24;
98; Conservative 45; Mismatches 102;
                                                                                                 Lowitz, Kevin P.
Behan, Dominic P.
      Leonard, James
                                     Hakak, Yaron
Liaw, Chen
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Best Local S:
Matches 98,
                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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ORGANISM:
                                 APPLICANT:
APPLICANT:
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94 NFGDIP-CRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLM 152
                                                                142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: Mifluence inflammatory conditions of chronic
TITLE OF INVENTION: inflammatory airway diseases
FILE REPERENCE: 082 000
CURRENT APPLICATION NUMBER: US/09/944,807
CURRENT FILING DATE: 2001-08-31
PRIOR PAPLICATION NUMBER: UK 0021484.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ii Score 369.5; DB 2; ii Pred. No. 2.7e-24; 45; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09944807
Patent No. 6773895
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35.0%;
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Best Local Similarity 35.0%
Matches 98; Conservative
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US-10-314-048A-135
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US-09-944-807-21
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LENGTH: 387
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Gaps

35;

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IITLE OF INVENTION: Coupled Receptor GPR1
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US-09-875-076-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LLGFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATR-KAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQQWTFTRIYMTNLAVADLC 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.3%; Score 360.5; DB 1; Length 3
29.2%; Pred. No. 1.4e-23;
tive 68; Mismatches 107; Indels
                                                                                                                                        SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGRET INFORMATION:
                                                                                                                                                                                                                                                                                                                                        1488.1140003/EKS/KLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08467947A Patent No. 6090575 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 148
                                                                                       MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                : 344 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 29.2
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             202-371-2540
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                                                                          COMPUTER READABLE FORM:
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     WASHINGTON
                                        USA
                                                        20002
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US-08-467-947A-8
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                                          COUNTRY:
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69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
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STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
COUNTY: DC
                                                                                                                                                                                                                                       MEDIUM TIEBE FUCKTION COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITH RELEASE #1.0, VERSION #1.30
SUSTRAKE: PATEMITH RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, REIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPRAK: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.3%; Score 360.5; DB 2;
illarity 29.2%; Pred. No. 1.4e-23;
Conservative 68; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                      COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
                     NUMBER OF SEQUENCES: 3
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Best Local Similarity
Matches 90; Conserva
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179 FSDBLWKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLA-RP--DATQSQRRRKTVRL 235
                                                                           219 WANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLSDANCCLDAI 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
ITILE OF INVENTION: Coupled Receptor GPR2
UNDMER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.3%; Score 359.5; DB 1; Length 302; 30.0%; Pred. No. 1.5e-23; tive 64; Mismatches 103; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1488.1140003/EKS/KLM
                                                                                                                                                                                                                              296 VYYFSAEGFRNTLRGLGTPHRAR 318
                                                                                                                                                                                          275 CYYYMAKEFQEA-SALAVAPRAK 296
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/08467948A Patent No. 5998164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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not relevant
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Matches 90; Conservative
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CAO, LIANG
NI, JIAN
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 RYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLV-----ARWLLGIQEGGFCFRS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 RYAAIVHPLRLRHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCFES 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
APPLICANT: Lin, I-Lin
ITILE REFERENCE: ARRNONGS
CURRENT APPLICATION NUMBER: US/09/675,076
CURRENT APPLICATION NUMBER: US/09/675,076
CURRENT PLILING DATE: 1999-10-12
PRIOR PRILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PLILING DATE: 1999-03-12
PRIOR PLILING DATE: 1999-03-12
PRIOR PLILING DATE: 1999-03-12
PRIOR PLILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/130,430
PRIOR PLILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/150,533
PRIOR PLILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/150,533
PRIOR APPLICATION NUMBER: 60/150,534
PRIOR APPLICATION NUMBER: 60/150,534
PRIOR APPLICATION NUMBER: 60/150,234
PRIOR APPLICATION NUMBER: 60/150,234
PRIOR APPLICATION NUMBER: 60/150,234
PRIOR PLILING DATE: 1999-00-129
PRIOR PLILING DATE: 1999-00-120
PRIOR PLILING DATE: 1999-00-120-13
PRIOR PLILING DATE: 1999-00-120-13
PRIOR PLILING DATE: 1999-00-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 33.7
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner. Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
FILE REFREENCE: 22 US6.CIP.
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT PILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 09/995,543
PRIOR FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 PL----COLSQGIYLINRYMSISLVTALAVDRYVAVRHPLRARGLRSPRQAAVCAVLWV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 LVIG----SLVARWILGIQEGGFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKVV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 TALAQRPPTDVGQAEATRKAKR---MVWANLLVFVVCFLPLHVGLTVRLAVGW----- 245
                                                                                                                                                                                                            278
                                                                                                                                                  110 STWKTYLSRIVIFIEIVGFFIPLILMVTCSTMVLRTL-NKPLTLSRNKLSKKKVLKMIFV 228
                                                                                                                                                                                                                                 120 KTLRTKRNARIVCVAVWITVLAGSTPASF------FQSTINRQNNTEQRICFENFPE 169
61 FVFTLPFRIYYF-VVRNWPPGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 119
                                                                                                                          177 ------LLGFYLPLAVVVFCSLKVVTALAQRPFTDVGQAEATRKAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 IGLEFVFGLIGNGLALMIFCFHLKSWKSSRIFLENLAVADFLLICLPFLTDNYVHNWDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDT
                                                                                                                                                                                                         222 NILVFVVCPLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY
                                             125 RGLRSPRQAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP-
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;; Pred. No. 1.7e-22;
43; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                   Sequence 137, Application US/10314048A Patent No. 6902902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.6%;
33.1%;
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SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.1%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lowitz, Kevin P.
Behan, Dominic P
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richman, Jeremy
Connolly, Daniel
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Hakak, Yaron
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Hakak, Ya.
Chen
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                                                                                                               170 STWKTYLSRIVIFIEIVGFFIPLILMVTCSTMYLRTL-NKPLTLSRNKLSKKKVLKMIFV 228
                                                                                                                                                                       NLLVEVVCFLPLHVGL----TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLINSLALWVFCCRMQQWTETRIYMTNLAVADLC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                    RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP- 176
                                                                                            ----LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLMLAISDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynuclectides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
F: 1100 NEW YORK AVE., NW, SUITE 600
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: TEMPER PLOSEY DISK
COMPUTER: IBM PC CONPATIBLE
COMPUTER: IBM PC CONPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATORNEY/AGENT INFORMATION:
NAME: STEPPE, ERIC K.
REGISTRATION NUMBER: 36,688
RESPERENCE/DOCKET UNBER: 1488.1140002/EKS/KLM
TELECOMMULCATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                RESULT 13
US-08-467-947A-30
is Sequence 30, Application US/08467947A,
patent No. 6090575
igeneral INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.0°
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CAO, LIANG
NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                              177
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
FILE OF INVENTION: for the Treatment of Metabolic-Related Disorders
FILE REFERENCE: 22.US6.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 WSLRQR------QMDRHAKIKRAINFINVVAIVFIICFLP---SVAVRIRIFWLLYKYNV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -VLHSLRD----TSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFR-----STRHNFNSMRFPLLG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 FYLPLAVVVFCSLKVVTALAORPPTDVGQABATRKAKRMVWANLLVFVVCPLPLHVGLTV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 PPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 340.5; DB 2; Length 351;
33.2%; Pred. No. 8e-22;
tive 48; Mismatches 114; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PPLLILAF-----LLGALGNGLALCGFCFHMKTWKSSTIYLFNLAVADFLLMICLPL
                                                                                          261 RNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSF 298
                                                               246 NACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT PEDLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-12-06
PRIOR PEDLICATION NUMBER: U0/096,511
PRIOR PILING DATE: 2002-03-12
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR APPLICATION NUMBER: 60/49,761
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
                                                                                                                                                                                                 Sequence 157, Application US/10314048A
Patent No. 6902902
GENERATION:
APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
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Best Local Similarity 33.2%
Matches 107; Conservative
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Leonard, James
Hakak, Yaron
Liaw, Chen
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US-10-314-048A-157
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Oy 292 AP----RAKAHKSOD----SLC 305

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| 306 KPRRPGRSQARRSEEMPISNLC 327

Search completed: February 9, 2006, 01:02:28
Job time : 34.5 secs
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20, Appl
492, App
84, Appl
351, Appl
44, Appl
44, Appl
176, App
176, App
116, Appl
11, Appl
11, Appl
116, Appl
116, Appl
116, Appl
116, Appl
116, Appl
1176, Appl
1177, Appl
1174, Appl
1174, Appl
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                                              9, 2006, 01:16:44; Search time 118.5 Seconds (without alignments) 1089.530 Million cell updates/sec
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/: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
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363 363 363 363 363 363 363 363 319 319 573 573		ULT 1 09-768-877-20 equence 20, Application US/0 atent No. US20020150895A1 EMERAL INPORMATION: APPLICANT: POLONSKY, KENNETH APPLICANT: POLONSKY, KENNETH APPLICANT: COX, NANCY J. APPLICANT: COX, NA	99. ilarity 99. Conservative	GSSDL GSSDL	NLAVADLCLLCTLP AVADLCLLCTLP	PLRARGLRSPROAAAVCAVLWVLVI
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		SULT 1 -09-768-877-20 Sequence 20, Application Patent No. US20020150896A GENERAL INFORMATION: APPLICANT: POLONSKY, KEN APPLICANT: POLONSKY, KEN APPLICANT: ODA, NAOHISA APPLICANT: COX, NANCY J APPLICANT: CHOI, KENIC APPLICANT: GTANI, KENIC APPLICANT: GTANI, KENIC APPLICANT: GTANI, KENIC APPLICANT: GTANI, KENIC APPLICANT: ARDICATION: METH FILE REFERENCE: ARCD: 30 CURRENT FILING DATE: 20 CURRENT FILING DATE: 1999- NUMBER OF SEQ ID NOS: 30 SOFTWARE: PATICATION NUMBER PRIOR FILING DATE: 1999- NUMBER OF SEQ ID NOS: 30 SOFTWARE: PATICATION	th Simila 108; Co	MNGTY 	NLAVA LAVA	PLRAR
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                                                                                                                                                                                                   Length 309;
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Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand
FILE REPRENENCE: P03-0006PCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT PILING DATE: 2004-08-20

PRIOR PILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: UP 2002-13949

PRIOR PILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 233
                              PatentIn version 3.1
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       NUMBER OF SEQ ID NOS: 3114
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US-10-696-639-44
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ORGANISM: Human
                           SOFTWARE: Pate
SEQ ID NO 44
LENGTH: 309
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| Sequence 492, Application US/10225567A
| Publication No: US2030113798A1
| Sequence 492, Application US/10225567A
| Publication No: US2030113798A1
| GENERAL INFORMATION:
| APPLICANT: LifeSpan Biosciences
| APPLICANT: Burmer, Glenna C. APPLICANT: Roush, Christine L. TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORG CURRENT PLING DATE: 2001-12-19
| PRIOR PELING DATE: 2001-12-19
| PRIOR PRIOR APPLICATION NUMBER: 60/257,144
| NUMBER OF SEQ ID NOS: 2292
| SOPTWARE: Patentin version 3.1
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Publication No. US20050037439A1
GENERAL INFORMATION:
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION:
PLICANT: BOURNER, MAUREEN J.
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME FILE REFERENCE: 01040/1
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT PILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 60/422,176
PRIOR FILING DATE: 2002-10-29
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBFQBASALAVAPRAKAHKS 300
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Pred. No. 6.9e-147;
0; Mismatches 1; Indels
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Best Local Similarity 99.7%;
Matches 308; Conservative (
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                                             301 ODSLCVTLA 309
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ORGANISM: Homo sapiens
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LENGTH: 309
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US-10-081-810-44

Sequence 44, Application US/10081810

Sequence 44, Application US/10081810

Sequence 44, Application OS USEQUENCE OS 
                                                                                             APPLICANT: BARBER, I.
APPLICANT: BARBER, M. G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3,
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3,
TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
FILE REFERENCE: D0042NP
CURRENT PAPLICATION NUMBER: 06/0236, 713
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 34.1%
Matches 103; Conservative
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                                                  HAWKEN, D.R.
                            RAMANATHAN,
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APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Excelov, A. V.
APPLICANT: Krukovskav, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REFERENCE: 2760-103
CURRENT PAPLICATION WUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 351
LENGTH: 309
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Publication No. US20030186360A1
GENERAL INFORMATION:
APPLICANT: FEDER, J. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 351, Application US/10157031; Publication No. US20030108890A1; GENERAL INFORMATION: APPLICANT: Baranova, A. V.
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ORGANISM: Homo sapiens
US-10-157-031-351
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US-09-964-821B-11
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US-10-157-031-351
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24.8%; Score 401; DB 4; Length 37:
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: Shuji MURANATSU
APPLICANT: Shuji MURANATSU
APPLICANT: Yukiko NaGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-13-26
PRIOR APPLICATION NUMBER: G0/258,315
PRIOR PILING DATE: 2000-13-26
PRIOR APPLICATION NUMBER: U2554018/2001
PRIOR PILING DATE: 2000-10-2-8
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-26
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR PILING DATE: 2001-08-26
PRIOR PILING DATE: 2001-08-26
PRIOR PRING DATE: 2001-08-26
PRIOR PRING DATE: 2001-08-26
PRIOR PRING DATE: 2001-03-26
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 176, Application US/10024298A Publication No. US20030143540A1 GENERAL INFORMATION:
APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
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SEQ ID NO 176
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Goichi HONDA
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CRGANISM: Homo sapiens
US-10-024-298A-176
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APPLICANT:
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Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT PAPLICANTON NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 44
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 225
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Matches 103; Conservative
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US-10-225-567A-225
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-225
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                                                                                                            LENGTH: 370
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44 AVYSVVFILGLITNSVSLFVFCFRRKGARSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
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24.8%; Score 401; DB 4; Length 37
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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Publication No. US20040081986A1

GENERAL INFORMATION:

APPLICAT: WATSUDA, Akio et al.

TITLE OF INVENTION: NF-kB ACTIVATING GENE
FILE REFERENCE: 1254-0229P

CURRENT APPLICATION NUMBER: US/10/617,217A

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: JP 2000-40228B

PRIOR APPLICATION NUMBER: JP 2001-088912

PRIOR FILING DATE: 2001-03-26

PRIOR FILING DATE: 2001-08-24
FILE KEFERENCE DOUGHER: US/10/268,332
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US. 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: U.S. 60/313,171
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PARENTIN VETSION 3.1
LENGTH: 370
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Sequence 11, Application US/10268332
Publication No. US20030175748A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: INVOICE HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHL
TITLE OF INVENTION: INVOICE HUMAN COLON- RELATED TISSUES
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28;
                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT APPLICATION NUMBER: JP 2000-4028B
PRIOR PILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-13-6
PRIOR PILING DATE: 2001-03-6
PRIOR PILING DATE: 2001-03-6
PRIOR PILING DATE: 2001-03-7
PRIOR PILING DATE: 2001-03-7
PRIOR PILING DATE: 2001-02-3
PRIOR PILING DATE: 2001-03-8
PRIOR PILING DATE: 2001-03-6
                                                                                                                                                                                                                                                                                                            APPLICANT: MATSUDA, Akio et al.
TITLE OF INVENTION: NFKB Activating Gene
                                                                                                                                                                                          US-10-042-211A-176
Sequence 176, Application US/10042211A
Publication No. US220030170719A1
GENERAL INFORMATION:
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US-10-042-211A-176
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     190 CSLKVVTALAQRPPTDVGQAEAT-RKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                                       249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQRASALAVAPRAKAHKSQDSLC 305
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24.8%; Score 401; DB 4; Length 379
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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APPLICANT: ASAHITKASEI KABUSHIKI KAISHA
APPLICANT: AALO MATSUDA
APPLICANT: AALO MATSUDA
APPLICANT: GOLCH HOUDA
APPLICANT: Shuji MURAMATSU
APPLICANT: Shuji MURAMATSU
APPLICANT: Shuji MURAMATSU
APPLICANT: Shuji MURAMATSU
TITLE OF INVENTION: NET & BACTIVALING Gene
FILE REPERENCE: 1254-0191P
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-28
SOFTWARE: PATENTIN VONS: 182
SOFTWARE: PATENTIN VONS: 182
SOFTWARE: PATENTIN VON: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 176, Application US/10024298A; Publication No. US20040214167A9; GENERAL INFORMATION:
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US-10-024-298A-176
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Publication No. US20040209808A1
GENERAL INFORMATION:
APPLICANT: Bristol-Wers Squibb Company
APPLICANT: Kornacker, Michael
ITILE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
FILE REPERENCE: DO286 NP
CURRENT APPLICATION NUMBER: US/10/775,965
CURRENT APPLICATION NUMBER: US. 60/446,655
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 370
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ORGANISM: Homo sapiens
US-10-775-965-11
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US-10-617-217A-176
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Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps
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DD 223 CSSVVLRTL.-RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPRNSVLFLYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQSASALAVAPRAKAHKSQDSLC 305

DD 281 TNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307

DD 335 KT 336
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3: /cgn2_6/ptodata/1/pubpaa/US07 NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIE

SUMMARIES	Query Score Match Length DB ID Description	-	6 US-10-055-877-248 Sequence 248,	.5 20.4 254 6	5 20.4 254 6 US-10-055-877-340 Sequence	.5 20.4 254 6 US-10-877-346-83 Sequence 83	.5 19.6 346 7 US-11-157-930-2 Seguence 2, Ap	5 19.5 365 6 US-10-995-561-545 Sequence 54	.3 391 7 US-11-127-877-52 Sequence	6 US-10-055-877-225 Sequence 22	18.6 259 6 US-10-055-877-237 Sequence 23	18.5 339 7 US-11-157-930-4 Sequence 4,	18.5 367 7 US-11-157-930-6 Sequence 6,	18.4 358 7 US-11-127-877-66 Seguence 66	18.4 373 7 US-11-127-877-46 Sequence 46	5 17.7 352 6 US-10-995-561-523 Sequence 52	5 17.7 352 7 US-11-068-686-2	5 17.7 352 7 US-11-127-877-61 Sequence 61	5 17.7 352 7 US-11-068-686-20 Seguence 20	5 16.9 337 7 US-11-157-930-5 Sequence 5,	5 16.9 375 7 US-11-127-877-67 Sequence 67	5 16.2 374 7 US-11-127-877-62 Sequence 62, 7	5 15.8 359 6 US-10-995-561-712 Sequence 712,	359 6 US-10-995-561-716 Sequence 716,	5 15.8 359 6 US-10-876-787-2 Sequence 2, Ag	2 15 0 250 7 112-11-127-65 Semience 65
		-	•	329.5	329.5	329.5	316.5	315.5	311.5	300	300	298	298	297.5	296.5	286.5	286.5	286.5	285.5	273.5	273.5	261.5	255.5	255.5	255.5	U
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Sequence 714, App	Sequence 715, App	Sequence 55, Appl	Sequence 934, App	Sequence 838, App	Sequence 837, App	Sequence 2, Appli	Sequence 60, Appl	Sequence 161, App	Sequence 4, Appli	Sequence 64, Appl	Sequence 4, Appli	Sequence 36, Appl	Sequence 12, Appl	Sequence 24, Appl	Sequence 636, App	Sequence 637, App	Sequence 6, Appli	Sequence 59, Appl	Sequence 32, Appl
US-10-995-561-714	US-10-995-561-715	US-11-127-877-55	US-10-821-234-934	US-10-995-561-838	US-10-995-561-837	US-11-216-610-2	US-11-127-877-60	US-10-055-877-161	US-11-068-686-4	US-11-127-877-64	US-11-216-610-4	US-10-959-310-36	US-11-218-281-12	US-11-218-281-24	US-10-995-561-636	US-10-995-561-637	US-11-216-610-6	US-11-127-877-59	US-11-218-281-32
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255.5	255.5	254	250	249	249	248.5	246.5	243.5	243.5	243.5	243.5	242.5	241	241	240.5	240.5	237.5	234.5	234.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
THER REPERRENCE: 21402-212
CURRENT APPLICATION NUMBER: US/10/055,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262, 892
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263, 598
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
Application US/10055877
o. US20050288241A1
                                                          APPLICANT: Decision Marc
APPLICANT: Pedigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tohernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Sarleh, Valerie
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
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Taupier Jr., Raymond
Pena, Carol
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Shimkets, Richard
Gusev, Vladimir
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Burgess, Cahterine
Bisen, Andrew
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Zerhusen, Bryan
Andrew, David
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RESULT 3
US-10-055-877-340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                    PEATURE:
1 OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
1 OTHER INFORMATION: transmembrane receptor domain
18-10-055-877-248
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PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,950
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 327, Application US/10055877 Publication No. US20050288241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DeCristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
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Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
Guo, Xlaojia
Zerhusen, Bryan
Andrew, Bryan
Mezes, Peter
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Burgess, Cahterine
Elsen, Andrew
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Baumgartner, Jason
Shimkets, Richard
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US-10-055-877-327
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APPLICANT: Boilday, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPERENCE: 2402-251

CURRENT APPLICATION NUMBER: 60/262, 897

FRIOR PLILING DATE: 2002-01-22

FRIOR APPLICATION NUMBER: 60/263, 598

FRIOR PLILING DATE: 2001-01-19

FRIOR PLILING DATE: 2001-01-24

FRIOR APPLICATION NUMBER: 60/264, 117

FRIOR PLILING DATE: 2001-01-24

FRIOR PLILING DATE: 2001-01-24

FRIOR PLILING DATE: 2001-01-24

FRIOR PLILING DATE: 2001-01-25

FRIOR APPLICATION NUMBER: 60/264, 139

FRIOR FILING DATE: 2001-01-26

FRIOR FILING DATE: 2001-01-26

FRIOR FILING DATE: 2001-01-26

FRIOR FILING DATE: 2001-01-26

FRIOR FILING DATE: 2001-01-36

FRIOR FILING DATE: 2001-01-36

FRIOR FILING DATE: 2001-03-14

FRIOR FILING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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Best Local Similarity 33.7%; Pred. No. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 LLETIR----RALYITSKLSDANCCLDAICY 276
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Vernet, Corine
Taupier Jr., Raymond
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ORGANISM: Artificial Sequence
                                                                                                                        Shenoy, Suresh
Li, Li
Casman, Stacie
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193 KVVTALAQRPPTDVG----QAEATRKAKRMVWANLLVPVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                144 V----IGSLVARWILGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                           : |: | || |: |
112 ALLISLPPLIFSWLRIVEEGNTIVCLIDFPEESVKRSY-VLLSTLVGFVLPLLVILVCYT 170
                                                                                                                                                                                                                                                                         171 RILATLRKRARSORSLKRRSSSERKAAKMILVVVVVFVLCWLPYHIVLLL-----DSLC 224
                            52 FGDALCKLVGALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVL 111
84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shimkets, A
APPLICANT: Beach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-28
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2000-10-05
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NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                  225 LLSIWRVLPTALLITLWLAYVNSCLNPIIY 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 83, Application US/10877346 Publication No. US20060014153A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ellerman, Karen
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
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Kekuda, Ramesh
Spytek, Kimberly A
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ORGANISM: Artificial Sequence
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
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CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT PILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: G0/262,892
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-23
PRIOR PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR PILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boldog, Ference
IIILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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20.4%; Score 329.5; DB 6; Length 254;
Best Local Similarity 33.7%; Pred. No. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps
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      DeCristofaro, Marc
Padigaru, Muralidhara
Miller, Charles
Tohernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
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Shimkets, Richard
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
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Burgess, Cahterine
Eisen, Andrew
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Zerhusen, Bryan
Andrew, David
                                                                                                                                                                                                                                                                                     Ratelli, Luca
Kekuda, Ramesh
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Mezes, Peter
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LENGTH: 254
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APPLICANT:
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APPLICANT:
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US-11-127-877-52

Sequence 52, Application US/11127877

Sequence 52, Application WS/11127877

Sequence 52, Application WS/11127877

Sequence 52, Application Worlds  

APPLICANT: Merchiers, Pascal G.

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  

TITLE OF INVENTION: Methods  

TITLE OF INVENTION: Methods  

TITLE OF INVENTION: Methods  

TITLE OF INVENTION: WHERE: US/11/127,877

CURRENT PILING DATE: 2005-05-12

PRIOR PILING DATE: 2004-05-12

PRIOR FILING DATE: 2004-05-12
                                                                                                                                                                                                                                   US-10-995-561-545

Sequence 545, Application US/10995561

Sequence 546, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CARDICANA DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: PRESENCE FREESOF OF Windows Version 4.0
:|||| | || || || || || 257 FLCFLPYHTLRTVHLTT-WKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 VVFVLGLGLNAPTLWLFIPRLRPWDATATYMFHLALSDTLYVLSLPTLIYYYAAHNHWPF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 IGSLVAR-WLLGIQEGG---FCFRSTR-----H--NFNSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 AGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLL-FGVPCLVTLVCYGL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 VVTALAORPPTDVGQAEATRKAK--RMVMANILIVPVVCPLPLHVGLTV----RLAVGWNA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 CALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQE-------ASALAV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 CRVLNIVNVVYKVTRPLASANSCLDPVLÝLLTGDKYRRQLRQLCGGGKPQPRTAASSLAL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP-
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29.2%; Pred. No. 3.2e-23;
tive 56; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 APRAK-----AHKSQDSLCVT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 VSLPEDSSCRWAATPODSSCST 359
                                                                                  286 -ASALAVAPRAKA 297
                                                                                                                                   316 LKSALRKGHPQKA 328
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; ORGANISM: Homo sapiens
US-10-995-561-545
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Best Local Similarity
Matches 94; Conservat
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                                                                                                                                                                                                                                                                 84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
                                                                                                                                                                                                                                                                                            144 V----IGSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                                                                                                                                                                                                                                                                          112 ALLLSLPPLLFSWLRTVEEGNTTVCLIDFPERSVRRSY-VLLSTLVGFVLPLLVILVCYT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 KVVTALAORPPIDVG---QAEATRKAKRMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TNLAVADLCLLCTLPF-VLHSLRDTS----DTPLCQLSQGIYLTNRYMSISLVTALAVDR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 SMRFP-----LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 YVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGG---FCFRSTRHNFN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 VVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQE- 285
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                                                                                                                                                         28 GVLLVLGLLLNSLALWVFCCRMOOWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T
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                                                                                                          Gaps
                                                                                                        37;
                                                 20.4%; Score 329.5; DB 6; Length 254; 33.7%; Pred. No. 9.5e-25; ive 54; Mismatches 88; Indels 37
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TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
FILE REPRENCE: 04974.0458
CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR FILING DATE: 2001-04-09
PRIOR PILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
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Best Local Similarity 28.4%; Pred. No. 2.4e-23;
Matches 89; Conservative 64; Mismatches 139; Indels
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                                                                                                     91; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                         Best Local Similarity
JS-10-877-346-83
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US-11-157-930-2
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                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                             165 STRHN------FINSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 BATRKAKRMVWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 TETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVT 108
                                                                                                                                                                                                                                                                                                                                                            AIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
                                                                                                                                                                                                                             1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVIGLLLNSLALWVFCCRMQQW 52
                                                                                                                                                                                                                                                           38 LNGTFAQSKCPQVEWLGWLNTIQPP-----FLWVLFVLATLENIFVLSVFCLHKSSC 89
                                                                                                                                                                                              51;
                                                                                                                                                               Length 391;
                                                                                                                                                              19.3%; Score 311.5; DB 7; Length 3 27.6%; Pred. No. 8.3e-23; Live 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 YSNSCLNPLVYVIVGKRFRKKS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 DANCCLDAICYYYMAKEFQEAS 287
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 225, Application US/10055877
Publication No. US20050288241A1
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APPLICANT: Decitatofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Spycek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Retelli, Luca
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Taupier Jr., Raymond
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Mezes, Peter
Patturajan, Meera
Burgess, Cahterine
Bisen, Andrew
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Gusev, Vladimir
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Zerhusen, Bryan
Andrew, David
                                                                                                                                                                                              Conservative
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                                                                                                                , ORGANISM: Homo sapiens
US-11-127-877-52
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Best Local Similarity
Matches 89; Conserv
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Boldog,
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APPLICANT:
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86 ----TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLR-SPRQAAAVCAVL 140
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CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT APPLICATION NUMBER: US/10/055,877
FURD APPLICATION NUMBER: G0/262,892
PRIOR PILING DATE: 2001-01-19
FRIOR PILING DATE: 2001-01-24
FRIOR APPLICATION NUMBER: G0/263,799
FRIOR APPLICATION NUMBER: G0/264,117
FRIOR APPLICATION NUMBER: G0/264,117
FRIOR PILING DATE: 2001-01-25
FRIOR PILING DATE: 2001-01-25
FRIOR PLING DATE: 2001-01-25
FRIOR PLING DATE: 2001-01-25
FRIOR APPLICATION NUMBER: G0/264,478
FRIOR APPLICATION NUMBER: G0/263,351
FRIOR APPLICATION NUMBER: G0/263,351
FRIOR PILING DATE: 2001-01-02
FRIOR PILING DATE: 2001-03-02
FRIOR APPLICATION NUMBER: G0/275,990
FRIOR PILING DATE: 2001-03-04
FRIOR PILING DATE: 2001-03-04
FRIOR PILING DATE: 2001-03-04
FRIOR FILING DATE: 2001-03-04
FRIOR FILIN
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IIILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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Miller, Charles
Tchernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
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APPLICANT: Padigaru, Muralidha
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Ballinger, Robert
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ORGANISM: Artificial Sequence
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Best Local Similarity 32.6%
Watches 92; Conservative
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US-10-055-877-237
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GFYLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRNVWANLLVFVVCFLPLHVGL- 237
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 88; Conserva
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APPLICANT: Boldog, Fercie

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2001-01-29

PRIOR PILING DATE: 2001-01-29

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-03-02

PRIOR PILING DATE: 2001-03-04

PRIOR PILING DATE: 2001-03-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 18.6%; Score 300; DB 6; Length 259;
1 Similarity 32.6%; Pred. No. 6.8e-22;
92; Conservative 49; Mismatches 85; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: 7tm_1 domain ; OTHER INFORMATION: consensus sequence US-10-055-877-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                  Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
                                                                                                                                                           Patturajan, Meera
Burgess, Cahterine
Eisen, Andrew
                                                                                                                                                                                                                                        Baumgartner, Jason
Shimkets, Richard
Gusev, Vladimir
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Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
                                                                            Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
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                                                                                                                                         Mezes, Peter
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Best Local Similarity
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LENGTH: 259
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APPLICANT:
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172 GFLIPLLVILVCYTRILRTL------RKAAKTLLVVVVVFVLCWLPYFIVLL 217
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                                                                                                                                                                                                                                                                                    Sequence 4, Application US/11157930

Sequence 4, Application US/11157930

Publication No. US20050266482A1

GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong

TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
FILE REFERENCE: 04974.00458

CURRENT APPLICATION NUMBER: US/11/157,930

CURRENT PILING DATE: 2005-06-22

PRIOR APPLICATION NUMBER: US/09/828,478

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 60/195,196

PRIOR FILING DATE: 2000-012-13

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 4.0

SEQ ID NO 4.0

SEQ ID NO 4.0
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29.1%; Pred. No. 1.46-21;
tive 54; Mismatches 128; Indels
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%Sequence 6, Application US/11157930

Publication No. US2005026482A1

%GENERAL INFORMATION:

APPLICANT: Xiao, Yonghong

7, TITLE OF INVENTION: Regulation of Human CyalIZ-Like GPCR

7, TITLE OF INVENTION:

FILE REFERENCE: 04974.00458
                                                                                        238 -- TVRLAVGWNA-CALLETIRRALYITSKLSDANCCLDAICY
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61; Gaps

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89; Conservative
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Sequence 66, Application US/11127877

publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiere, Pascal G.

APPLICANT: Spitterels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE REFERENCE: P27, 800-B USA

CURRENT APPLICATION UNMERR: US/11/127,877

CURRENT APPLICATION NUMBER: 60/570,352

PRIOR PILING DATE: 2004-05-12

PRIOR FILING DATE: 2004-06-12

PRIOR FILING DATE: 2004-06-24

NUMBER OF SEQ ID NOS: 590

SOUTHARE PATENTING PATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOUTHARE PATENTING PATE: 2004-08-24

SOUTHARE PATENTING PATE: 2004-08-24
                                                                                                                                                                                                                                                                                                                                                              64 VADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISLVTAIAVDRYVAVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                              |||| : || || : || || :| || 103 VADISCVLVLPTRIVYHPSGNHWPFGEIACRLTGFLFYIAMYASIYPLTCISADRFLAIV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 HPLRARGLRSPRQAAAVCAVLWVLVIGS----LVARWLLGIQEGGFCF----RSTRHNF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVG---QAEATRKAKRMVWANLLVFV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 VCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQ 284
                                                                                                                                                                                                                                                                                                                                           4 TYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLA 63
                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                        18.5%; Score 298; DB 7; Length 367; 29.1%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                             54; Mismatches 128; Indels
CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR PELLING DATE: 2000-12-13
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                            Query Match 18.5
Best Local Similarity 29.1
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-127-877-66
                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-11-157-930-6
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US-11-127-877-66
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LENGTH: 358
                                                                                                                                                                                             LENGTH: 367
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                                                                                                                                                                           SEQ ID NO 6
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Score 297.5; DB 7; Length 358; Pred. No. 1.7e-21;

18.4%;

Query Match Best Local Similarity

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SLVTAIAVDRYVAVRHPIRARGIRSPRQAAAVCAVLWVLV---IGSLVARWLLGIQEGG- 160
                                                                                                                                                                                                                                                                              | : | : | : | : | CR-----VFALTVLEFILPLLVISVFTGRIMCALSR--PGLLHQGRQRRVRAMQLLLT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOGWTETRIYMTNIAVADLCLLCTLPPVLHSLRDTSD----TPLCQLSQGIYLTNRYMSI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 -PCFRSTRHNF-----NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 ITCYDTTSDBYLRSYFIYSMCTTVAMFCVPLVLILGCYGLIVRALIYK---DLDNSPLRR 256
                                                                                                                                                                               SISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFC 162
                                                                                                                                                                                                     163 FRSTRHNFNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAKRMVWA 221
                                                                                                                                                                                                                                                                                                                              222 NLLVEVVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAK 281
                                                                                                                                                                                                                                                                                                                                                      |::|:|| | | | ::
246 VLIIFLVCFTPFHAR---QVAVALWPDMPHTTSLVVYHVAVTLSSLNSCMDPIVYCFVTS 302
                                                                                                      61 NLAVADL-------CLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM 102
                                                                                                                                           94 NLVVTDLLVGLSLPTRFAVYYGARGCLRCAFPHVLG-------YFLNMHC 136
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                                                  45 LHGTF------PGLCVALMAVHGAIFLAGLVLNGLALYVFCCRTRAKTPSVIXTI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GTYNTCGSSDLTWPPAI-----KLGF-YAYLG----VLLVLGLLILNSLALWVFCCR
                                1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALMVFCCRMQQWTETRIYMT
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42; Mismatches 111; Indels
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                                                                                                                                                                                                Sequence 523, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE OF INVENTION: DETECTION AND USES THEREOF
FILE OF INVENTION: UNDER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 523
214 KAKRMVWANILLVFVVCFLPLHVGLTVRLAVGWN----ACALLETIRRALYITSKLSDAN 268
                       75 PVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 LPLLVMVICYSGILKTLLR-----CRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNT 259
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| Publication No. US20505026055A1
| GENERAL INFORMATION:
| APPLICANT Gray, Patrick W. Schweickart, Vicky L. |
| TITLE OF INVENTION: Chemokine Receptor Materials and Methods |
| TITLE OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESS: | ABLEBELL |
| ABDRESSEE: MAISBALL |
| STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%; Score 286.5; DB 6; Length 352; 26.2%; Pred. No. 1.9e-20; ative 62; Mismatches 118; Indels 31;
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                                                                           269 CCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSL 304
                                                                                               317 SCVDPILYFLAGDTFRR--RLSRATRKASRRSEANL 350
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 26.4..
Local Similarity 26.4..
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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75 FVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AAAVCAVLWVL-VIGSLVARWLLGIQEGGPCFRSTRH------NFNSMRFPLLGFY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 GVVTSVITWVVAVFASLPGIIFTRSQKRGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLV 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%; Score 286.5; DB 7; Length : 26.2%; Pred. No. 1.9e-20; tive 62; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /= "88C amino acid sequence" SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/068,686
FILING DATE: 28-Feb-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REPRENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-474-630
TELEFAX: 312-474-630
TELEFAX: 312-474-630
TELEFAX: 312-474-630
TELEFAX: 312-474-630
TELEFAX: 312-474-630
TYPE: amino acids
TYPE: amino acids
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 26.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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Sequence 20, Appl Sequence 492, App Sequence 351, Appl Sequence 11, Appl Sequence 11, Appl Sequence 176, App Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 116, App Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 114, Appl Sequence 114, Appl Sequence 117, Appl Sequence
                                                                                                                                                                                                         ; Search time 118.5 Seconds (without alignments)
1089.530 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                             US-10-083-168-16
1614
1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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Sequence 1
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Sequence
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1. /cgn2_6/ptodata/1/pubpa/USO2_PUBCOMB.pep:*

2. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

3. /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

4. /cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

5. /cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

5. /cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

5. /cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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US-10-225-567A-492

US-10-269-639-44

US-10-157-031-351

US-09-964-821B-11

US-10-091-81-44

US-10-025-567A-225

US-10-024-298A-176

US-10-268-332-11

US-10-024-298A-176

US-10-024-298A-176

US-10-024-298A-176

US-10-024-298A-174

US-10-031-318-178-174

US-10-031-318-159

US-10-314-048A-159

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US-10-314-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                        9, 2006, 01:16:44
                                                                                                                                                model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                38
                                                                                                                                                protein search, using
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seq length: 200000000
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                                     Copyright
                                                                                                                                                                                                                        February
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Match
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Perfect score:
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Maximum DB
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		DIABETES	Length	WVFCCR 	SISLVT
25		N	·· in ··	LNSLAL        LNSLAL	LTNRYM        LTNRYM
US-10-619-141-19 US-10-167-192-1 US-10-167-192-1 US-10-400-991-4 US-10-400-991-4 US-10-505-486-45 US-10-321-807-36 US-10-321-807-36 US-10-321-807-36 US-10-321-807-36 US-10-31-807-36 US-10-997-815-36 US-10-997-815-36 US-10-997-815-36 US-10-997-815-36 US-10-997-815-36 US-10-907-815-36	īS	OF TYPB	4; DB 3 1.2e-14 hes 0	LVLGLL         LVLGLL	LSQGIY          LSQGIY
10 - 6.19 - 14.19.19.19.19.19.19.19.19.19.19.19.19.19.	ALIGNMENTS	ENT , 877	ore 1614; ed. No. 1. Mismatchee	AYLGVL         AYLGVL	DTPLCQ        DTPLCQ
US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US-10- US	AL		Sc. Pr	IKLGFY        IKLGFY	SLRDTS         SLRDTS
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		ULT 1  09-768-877-20  atence 20. Application US/09768977  atent No. US20020150896A1  ENERAL INFORMATION:  APPLICANT: POLONSKY, KENNETH S.  APPLICANT: POLONSKY, KENNETH S.  APPLICANT: COX, NANCY J.  APPLICANT: COX, NANCY J.  APPLICANT: COX, NANCY J.  APPLICANT: COX, NANCY J.  APPLICANT: SREMAN, SEAMUS  APPLICANT: COX, NANCY J.  APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: BLL, GRAME I.  TITLE OF INVERTION: METHODS OF TREA  FILE REFERENCE: ARCJ. 307  CURRENT APPLICATION NUMBER: US/02/2, 86  PRIOR FILING DATE: 1999-10-21  RUMBER OF SEQ ID NOS: 30  SOFTWARE: PATENTIN VET. 2.0  LENGTH: 309  LENGTH: 309  LENGTH: 309  LENGTH: BRT  ORCANISM: Human	vat.	SSDLT	LCTLPE 
,		-20 ORMATION: POLONSKY, KE POLONSKY, KE POLONSKY, KE HORIGAMA, Y ODA, NACHIS, COX, NANCY SREENAM, SE ZHOU, YUN-P CATAMI, KENI HANIS, CRAIM BELL, GRAEM NUENCTION: BECKE: 2 HANIS, CRAIM OF LING DATE: 1999 SEQ ID NOS: 3 Patentin Ver. 09	Similarity 9; Conser		13 13 13 13 13 13 13 13 13 13 13 13 13 1
		-20 DEMALICATION DE LING DE LEGATION DE LING D	mila Co	NGTY 	#==# #==#
		7-20 00, 1 00, 1 0	ch 1 Sir 309;	Z—Z	N — N
376 376 376 376 376 3775 3775 3775 3775		SULT 1  -09-768-877-20  Genence 20, Application U  GENERAL INPORMATION:  GENERAL INPORMATION:  APPLICANT: POLONSKY, KENN  APPLICANT: POLONSKY, KENN  APPLICANT: OTAM, NACHISA  APPLICANT: COX, NANCY J.  APPLICANT: COX, NANCY J.  APPLICANT: SERENAN, SERM  APPLICANT: CHON, VIN-PIN  APPLICANT: APPLICANT: CHON, NUN-PIN  APPLICANT: APPLICANT: CHON, CRAICH  APPLICANT: BELL, GRAENE  FILE REFERENCE: ACCI:30  CURRENT FILING DATE: 1999-1  NUMBER OF SEQ ID NOS: 30  SOFTWARE: PALCHIN VET. 2  SEQ ID NO 20  LENGTH: 309  TYPE: PRIMMAN  CRANISM: Human  ORGANISM: Human	/ Mat Loca les		
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 US-09-768-877-20 Sequence 20, A Sequence 20, A Sequence 20, A Defect No. US-2 GENERAL INFORM APPLICANT: PO APPLICANT: CAPPLICANT: CAPPLICANT: CAPPLICANT: CAPPLICANT: CAPPLICANT: CAPPLICANT: CAPPLICANT: B APPLICANT: CAPPLICANT: B APPLICANT: CAPPLICANT: B APPLICANT: CAPPLICANT: B APPLICANT: B APP	Query M Best Lo Matches	& 8	B &

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; Pred. No. 1.2e-145;
0; Mismatches 0;
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Publication No. US20050118639A1
GENERAL INFORMATION
APPLICANT: Takeda Chemical Industries, Ltd.
ITILE OF INVENTION: Determination of a ligand
FILE REPERBENCE: P03-0006PCT
CURRENT PILING DATE: 2004-08-20
PRIOR PILING DATE: 2002-02-22
PRIOR PLICATION NUMBER: JP 2002-45728
PRIOR PILING DATE: 2002-07-23
PRIOR PILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-11
NUMBER OF SQ ID NOS: 233
LENGTH: 547
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                  100.0%;
NUMBER OF SEQ ID NOS: 3114
SOFTWARE: Patentin version 3.1
SEQ ID NO 44
LENGTH: 309
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Best Local Similarity 100.0
Matches 309; Conservative
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Matches 308; Conservative
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                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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US-10-505-486-84
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                                                                                                                                                                                             Sequence 492, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REPRENCE: 1920-4-4
CURRENT PILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
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Publication No. US20050037439A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION: DIFFRENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME;
FILE REPERENCE: 01040/1
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT PILING DATE: 2003-10-29
PRIOR PILING DATE: 2003-10-29
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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100.0%; Score 1614; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 309; Conservative 0; Mismatches 0; Indels 0
                                                                               301 QDSLCVTLA 309
                                            QDSLCVTLA 309
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ORGANISM: Homo sapiens
                                                                                                                                                                                  10-225-567A-492
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US-10-696-639-44
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LENGTH: 309
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Sequence 44, Application US/10081810

Publication No. US20030064438A1

GENERAL INFORMATION:
APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI
TITLE OF INVENTION: USES THERROF
FILE REFERENCE: D0132 NP
CURRENT APPLICATION NUMBER: US/10/081,810
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,793
PRIOR FILING DATE: 2001-02-3
PRIOR FILING DATE: 2001-02-06-06
                                APPLICANT: HAWKEN, D.R.
APPLICANT: CACACE, A. A. APPLICANT: CACACE, A. APPLICANT: CACACE, A. APPLICANT: CACACE, A. APPLICANT: CACACE, M. G. APPLICANT: CACACE, M. G. APPLICANT: CARRACKER, M. G. TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES FILE REFERRACE: D0042NP CURRENT FILING DATE: 2002-06-10
CURRENT APPLICATION NUMBER: 60/235,713
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2001-01-17
PRIOR PLLING DATE: 2001-01-17
PRIOR PLLING DATE: 2001-07-13
PRIOR PLLING DATE: 2001-07-13
PRIOR PLLING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 63
SOPTWARE: PALENTIN VET: 2.1
SEQ ID NO 11
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24.9%; Score 402; DB 3; Length 370
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
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s
                   RAMANATHAN, C.
HAWKEN, D.R.
CACACE, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-964-821B-11
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APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Kozlov, A. P.
APPLICANT: Kozlov, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences plus Repressor: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTHARE: PatentIn version 3.1
SEQ ID NO 351
LENGTH: 309
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                                                                                       241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLJVLGLLLNSLALWVFCCRMQOWTETRIYMT
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                                                                YLPLAVVVPCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGLTVR
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99.4%; Pred. No. 1.6e-144;
iive 0; Mismatches 2;
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US-09-964-821B-11
; Sequence 11, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 351, Application US/10157031; Publication No. US20030108890A1
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CORGANISM: Homo sapiens
US-10-157-031-351
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163 WILVLSGGISASLESTINVNNATTICEGGESKRVWKTYLSKIIIFIEVVGFIIPLILINVS 222
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                                                                                                                                                                                                                        281 INCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
                                                                                190 CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
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                                                                                                            223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAI
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Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
APPLICANT: ACIO, MATSUDA
APPLICANT: Golchi HONDA
APPLICANT: Shuji MURAMATSU
APPLICANT: Shuji MURAMATSU
APPLICANT: YUKIKO NAGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
FRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-26
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR APPLICATION NUMBER: 00/268,315
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-12-28
PRIOR FILING DATE: 2001-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 176, Application US/10024298A Publication No. US20030143540A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-024-298A-176
                                                                                                                                                                                                                                                                                             306 VT 307
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US-10-024-298A-176
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Publication Nb. US20030113798A1
GENERAL INPORMATION:
MEDICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFRENCE: 1920-4-4
CURRENT PELLING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOSTWARE: Patentin version 3.1
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24.9%; Score 402; DB 4; Length 370;

Best Local Similarity 34.1%; Pred. No. 8.2e-30;

Matches 103; Conservative 60; Mismatches 111; Indels 28;
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                        SOFTWARE: Patentin version 3.0 SEQ ID NO 44
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Best Local Similarity 34.1*
Matches 103, Conservative
  NUMBER OF SEQ ID NOS: 58
                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-225
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US-10-225-567A-225
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                                                                                LENGTH: 370
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82 -DTSDTBLCQLSQCIYLTNRYMSISLVTALAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140
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CURRENT APPLICATION NUMBER: US/10/617,217A CURRENT FILING DATE: 2003-07-11
PRIOR PELING DATE: 2000-12-28
PRIOR FILING DATE: 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/254018
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-24
              CURRENT APPLICATION NUMBER: US/10/268,332
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US. 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: U.S. 60/313,171
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-26
NUMBER: OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VETRION 3.1
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FILE REFERENCE: D0042A CIP
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Best Local S
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US-10-268-312-11
US-10-268-312-11
FUBLICATION NO. US20030175748A1
GENERAL INFORMATION:
A APPLICAT: BISTSOL SQUIDD Company
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
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                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT FILING DATE: 2002-01-11
PRIOR PILING DATE: 2000-12-28
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-02-4
PRIOR FILING DATE: 2001-02-4
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 176
                                                                                                                                                                                                                                                                                                                  APPLICANT: MATSUDA, Akio et al.
TITLE OF INVENTION: NFKB ACLIVATING Gene
                                                                                                                                                                                                     US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
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CORGANISM: Homo sapiens
US-10-042-211A-176
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104 WPPGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRSRTIFTRRNSAIVCAGV 162
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  CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                    249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSLC 305
                                                                                                                                 25 AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
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APPLICANT: Shuji MURAMATGU
APPLICANT: Shuji MURAMATGU
TITLE OF INVENTION: NP-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/214,385
PRIOR PILING DATE: 201-03-26
PRIOR FILING DATE: 201-03-26
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-03-26
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PRIOR PILING DATE: 2001-03-26
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PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-28
NUMBER: OF SEQ ID NOS: 182
SEQ ID NO 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ASAHI KASBI KABUSHIKI KAISHA
APPLICANT: Akio MATSUDA
                                                                                                                                                                                                                                                                                                                                                                         Sequence 176, Application US/10024298A Publication No. US20040214167A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goichi HONDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-024-298A-176
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Publication No. US20040209808A1
GENERAL INFORMATION:
APPLICANT: Bristol-W. Michael
TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
FILE REPRENCE: DO268 NP
CURRENT APPLICATION NUMBER: US/10/775,965
CURRENT PILING DATE: 2004-02-10
PRIOR FILING DATE: 2003-02-11
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENTIN VERSION 3.2
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24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels
SOFTWARE: Patentin Ver. 2.0
                                                                                               ; ORGANISM: Homo sapiens
US-10-617-217A-176
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ORGANISM: Homo sapiens
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                       SEQ ID NO 176
LENGTH: 370
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APPLICANT: DOROGHUE, MATY A.
APPLICANT: DOROGHUE, MATY A.
APPLICANT: DOROGHUE, MATY A.
APPLICANT: SOCITION: MATHODS AND COMPOSITIONS FOR TREATING
APPLICANT: TOMITHOON, James B.
TITLE OF INVENTION: MATHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 1669, 1228, 6350, 9015, 1802, 2365, 7301, 8955, 7301, 8955, 71112 OF INVENTION: 1669, 1228, 6350, 9015, 1802, 2365, 7301, 8016, 7112 OF INVENTION: 1669, 1228, 6350, 9015, 1802, 23652, 7301, 8016, 7112 OF INVENTION: 3533, 9462, 9135, 1230, 1729, 65552, 1241, 2147, 3170, 71712 OF INVENTION: 9180, 2569644, 13556, 53656, 44143, 32612, 10671, 261, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408, 71712 OF INVENTION: WINDER: US 60/445, 168
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-03-12
PRIOR PILING DATE: 2003-05-08
PRIOR PILING DATE: 2003-06-10
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Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps
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                                                                                                         APPLICANT: Millennium Pharmaceuticals, Inc.
Sequence 86, Application US/10753267
Publication No. US20050037946A1
                                                                                                                                          Stagliano, Nancy E.
Healy, Aileen
Acton, Susan L.
Galvin, Katherine M.
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; ORGANISM: Homo Sapiens
US-10-753-267-86
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	55-8	55-8	55-8	77-3	57-9	35-5	27-8	55-8	55-8	157-930-4	1-157-930-6	1-127-877-46	27-8	95-5	9-89	1-127-877-6	9-89	57-9	127-877-67	27-B	995-561-7	995-5	16-7	27-8	95-5
	0-0	-0	10-055-877-3	10-877-346-83	11-157-930-2	10-995-561-54	US-11-127-877-52	JS-10-055-877-225	US-10-055-877-2	1-1	1-1	1-1	US-11-127-877-66	US-10-995-561-52	9-1	1-1	US-11-068-686-20	US-11-157-930-5	4	US-11-127-877-6	6	-10-9	US-10-876-787-2	-11-127-877-65	-10-995-
e i	US-10-055-877	US-10-055-877-32	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	US-1	us-1
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& Query Match	20.7	20.7	20.7	20.7	19.7	9.5	9.4	8.9	8.9	9.8	8.6	8.5	18.4	7.9	7.9	7.9	7.8	7.1	6.8	6.3	5.8	5.8	5.8	5.8	5.8
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Score	5.5	5.5	5.5	5.5	7.5	5.5	312.5	305	305	300	300	298.5	297.5	288.5	288.5	288.5	287.5	275.5	270.5	3.5	5.5	5.5	55.5	5.5	5.5
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Result No.	1	7	m	4	Ŋ	9	7	89	٥	٢	1	12	13	14	15	16	17	18	19	20	21	22	23	24	25
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Sequence 714, App Sequence 715, App Sequence 55, Appl Sequence 934, Appl		6 4 4 6 4 A	Sequence 36, Appl Sequence 636, App Sequence 637, App Sequence 12, Appl Sequence 24, Appl	Sequence 6, Appli Sequence 59, Appl Sequence 32, Appl
US-10-995-561-714 US-10-995-561-715 US-11-127-877-55 US-11-123-4-934	US-11-216-610-2 US-10-995-561-838 US-10-995-561-837 US-10-055-877-161	US-11-127-877-60 US-11-068-686-4 US-11-127-877-64 US-11-216-610-4	US-10-959-310-36 US-10-995-561-636 US-10-995-561-637 US-11-218-281-12 US-11-218-281-24	US-11-216-610-6 US-11-127-877-59 US-11-218-281-32
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255.5 255.5 255	250 249 249	248.5 245.5 245.5	244.5 241.5 241.5 241 241	239.5 235.5 235.5
26 27 28	0 1 2 2	33 33 34 34 34 34 34 34 34 34 34 34 34 3	38 39 44 42 42	444 454 45

## ALIGNMENTS

APPLICANT: Boldog, Perence TILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby FILE REFERENCE: 21402-251 CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 0(0/262,892
PRIOR PELING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR PILING DATE: 2001-01-23
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25 Sequence 248, Application US/10055877 Publication No. US20050288241A1 GENERAL INFORMATION: Baumgartner, Jason Shimkets, Richard Gusev, Vladimir Vernet, Corine Taupier Jr., Raymond Pena, Carol APPLICANT: DeCristofaro, Marc APPLICANT: Padigaru, Muralidhara APPLICANT: Miller, Charles Zhong, Mei Anderson, David Ballinger, Robert Gerlach, Valerie Syrek, Kimberly Ratelli, Luca Kekuda, Ramesh Patturajan, Meera Burgess, Cahterine Ichernev, Velizar Guo, Xiaojia Zerhusen, Bryan Andrew, David Shenoy, Suresh Stacie Eisen, Andrew Li, Li Casman, Andrew, Wolenc, APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT

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112 ALLLSIPPLIFSWIRTVERGNITVCLIDFPERSVKRSY-VILSTLVGFVLPLIVILVCYT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T 83
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-36
PRIOR PLING DATE: 2001-03-01
PRIOR PLING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2011-03-14
PRIOR 
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20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7 ; OTHER INFORMATION: transmembrane receptor domain US-10-055-877-248
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APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
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Burgess, Cahterine
Eisen, Andrew
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ORGANISM: Artificial Sequence
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Baumgartner, Jason
Shimkets, Richard
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Andrew, David
Mezes, Peter
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, Ramesh
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Kekuda,
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US-10-055-877-327
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112 ALLLSLPPLLFSWLRTVEEGNTTVCLIDFPEESVKRSY-VLLSTLVGFVLPLLVILVCYT 170
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APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT PILING DATE: 2002-01-22

PRIOR PELLING DATE: 2001-01-29

PRIOR PELLING DATE: 2001-01-02

PRIOR APPLICATION NUMBER: 60/263,598

PRIOR PILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 60/263,799

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR PILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,139

PRIOR PILING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-04

PRIOR PLING DATE: 2001-03-04

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14
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Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: 7tm 1, 7 OTHER INFORMATION: transmembrane receptor domain consensus sequence
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US-10-055-877-340
Sequence 340, Application US/10055877
Publication No. US20050288241A1
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Li, Li
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52 PGDALCKLVGALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVL 111
                                                                                               144 V----IGSLVARWILGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
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112 ALLLSIPPLIFSWIRTVEBGNITVCLIDFPEBSVKRSY-VLLSTLVGFVLPLLVILVCYT 170
                                                                                                                                                                                                    193 KVVTALAQRPPIDVG---QAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                  84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL
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APPLICANT: Shinkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
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OTHER INFORMATION: Description of Artificial Sequence: 7
OTHER INFORMATION: transmembrane receptor Consensus Sequence
                                                                                                                                                                                                                                                                                                                                          225 LLSIWRVLPTALLITLWLAYVNSCLNPIIY 254
                                                                                                                                                                                                                                                                                                            250 LLETIR---RALYITSKLSDANCCLDAICY 276
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CURRENT PEDILICATION NUMBER: US/10/877,346
CURRENT PILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-877-346-83; Sequence 83, Application US/10877346; Sequence 83, Application No. US20060014153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgess, Catherine E
Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly A
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Blerman, Karen
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GNLLVILVILKTKKL-----RTPTNIFLLNLAVADLLFLLTLPPWALYYLVGGDWV 51
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APPLICANT: Boldog, Ference
IITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 340
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILLE KEKEKENCE: 1404C-251
CURRENT PELLING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 00/262,892
PRIOR PILING DATE: 2002-01-29
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-23
PRIOR PELLING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-04
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
ATT. Decritorian Marc
NT: Dedigaru, Muralidhara
NT: Miller, Charles
NT: Atlanew, Velizar
NT: Zhong, Mei
NT: Anderson, David
NT: Ballinger, Robert
NT: Spytek, Kimberly
NT: Ratelli, Luca
NT: Kekuda, Ramesh
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Taupier Jr., Raymond
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Shimkets, Richard
Gusev, Vladimir
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Burgess, Cahterine
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Zerhusen, Bryan
Andrew, David
Mezes, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolenc,
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APPLICANT:
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US-11-127-877-52

Sequence 52, Application US/11127877

Sequence 52, Application US/11127877

Sequence 52, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Goffmann, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27, 800-B USA

CURRENT APPLICATION NUMBER: US/11/127,877

CURRENT FILING DATE: 2006-05-12

PRIOR PILING DATE: 2006-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLL-FGVPCLVTLVCYGL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 VVTALAQRPPTDVGQAEATRKAARMVWANILVFVVCFLPLHVGLTV----RLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 MARRIYQ-PLPGSAQSSSRLRSIRTIAVVLTVFAVCFVPFHITRTIYYLARLLEA--DCR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| : :| |: || || || || 280 VLNIVNVVYKVTRPIASANSCLDPVLYLLITGDKYRRQLRQLCGGGKPQPRTAASSLALVS 339
88 ---LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 IGSLVAR-WLLGIQEGG---FCFRSTR----H--NFNSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 LLETIRRALYITSKLSDANCCLDAICYYYMAKERQE-------ASALAVAP 293
                                                                                                                                                                                                                             Sequence 545, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NOWER: US/10/995,561
SOURCENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 VVFVLGLGLARAPTLMLFIFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYAAHINHWPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 VILVLGLILINSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
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19.5%; Score 315.5; DB 6;
Best Local Similarity 29.1%; Pred. No. 2.3e-23;
Matches 93; Conservative 55; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 LPEDSSCRWAATPQDSSCST 359
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                                                                                                                   316 LKŚALRKGHPOKA 328
                                                                   286 -ASALAVAPRAKA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                       RESULT 6
US-10-995-561-545
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LENGTH: 365
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112 ALLLBLPPLLFSWLRTVEEGNTTVCLIDPPEESVKRSY-VLLSTLVGFVLPLLVILVCYT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 VVCPLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEPQE- 285
                                                                                                                                                                                                                                                               52 FGDALCKLVGALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVL 111
                                                                                                                                                                                                                                                                                                                                144 V----IGSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFPLLGFYLPLAVVVFCSL 192
                                                                                                                                                                                                                                                                                                                                                                                                                         193 KVVTALAQRPPTDVG---QABATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNACA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TNLAVADLCLLCTLPF-VLHSLRDTS----DTPLCQLSQGIYLTNRYMSISLVTAIAVDR 114
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                                                                                                                                                                                                                                    84 SDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVL 143
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                                                                                                                                                                                       21
                                                                                                                                           28 GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTL-PFVLHSLRD---T 83
                                                                                                                                                                      NGTYNTCGSSDLTWPPAIKLGFY--AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYM
                                                                                             Gaps
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                                                                                             37,
                                           20.7%; Score 334.5; DB 6; Length 254; 34.1%; Pred. No. 2.2e-25; ive 54; Mismatches 87; Indels 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
FILE RPERENCE: 04974.00458
CURRENT FILING DATE: 2005-06-22
CURRENT FILING DATE: 2005-06-22
PRIOR PILING DATE: 2001-04-09
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaelSEQ for Windows Version 4.0
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19.7%; Score 317.5; DB 7; Length 3
Best Local Similarity 28.4%; Pred. No. 1.4e-23;
Matches 89; Conservative 64; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 LLETIR --- RALYITSKLSDANCCLDAICY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/11157930; Publication No. US20050266482A1; GENERAL INFORMATION:
                                                                   34.1%;
                                                                                             92; Conservative
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                                                                        Best Local Similarity
    US-10-877-346-83
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US-11-157-930-2
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                                                                                                                                                                                                                                                                                                                                                                                                               150 LVSIDRYLALVKTMSMGRWRGVRWAKLYSLVIWGCTLLLSSPMLVFRTWKEYSDEG---- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 STRHIN------FINSMRPPLLGFYLPLAVVVFCSLKVVTALAORPPTDVGQA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATRKAARMVWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLS 265
                                                                                                                                                                                                                                                                                                                   53 TETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSISLVT 108
                                                                                                                                                                                                                                                                                                                                                                                       109 AIAVDRYVAVRHPLRARGLRSPROAAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 QTERRATVLVILVILLFIICWLPPQISTFLDTLHRLGI-LSSCQDERIIDVITQIASFMA 321
                                                                                                                                                                                                                                                                                38 INGTFAQSKCPQVEWLGWINTIQPP-----FLWVLFVLATLENIFVLSVFCLHKSSC 89
                                                                                                                                                                                                                                                 1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQOW 52
                                                                                                                                                                                                              51;
                                                                                                                                                                               Length 391;
                                                                                                                                                                             19.4%; Score 312.5; DB 7; Length 3 27.6%; Pred. No. 4.9e-23; tive 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 DANCCLDAICYYYMAKEFQEAS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 YSNSCLNPLVYVIVGKRFRKKS 343
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 52
LENGTH: 391
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APPLICANT: Dedrigtofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Ratelli, Luca
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
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Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
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Patturajan, Meera
Burgess, Cahterine
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Shimkets, Richard
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Zerhusen, Bryan
Andrew, David
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Wolenc, Adam
                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-52
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 89; Conserva
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Boldog, 1
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US-10-055-877-225
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86 ----TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLR-SPRQAAAVCAVL 140
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                                  | CHALES REFERENCE: A140Z-251
| CURRENT PELICATION NUMBER: US/10/055,877
| CURRENT PILLING DATE: 2002-01-22
| PRIOR APPLICATION NUMBER: 60/262,892
| PRIOR PELING DATE: 2001-01-19
| PRIOR PELING DATE: 2001-01-23
| PRIOR PELING DATE: 2001-01-25
| PRIOR PELING DATE: 2001-01-26
| PRIOR PELING DATE: 2001-01-30
| PRIOR PELING DATE: 2001-01-30
| PRIOR PELING DATE: 2001-03-34
| PRIOR PELING DATE: 2001-03-14
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1 Similarity 33.0%; Pred. No. 1.6e-22;
93; Conservative 49; Mismatches 84; Indels
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Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: DeCristofaro, Marc
APPLICANT: Padigaru, Murcalidhara
APPLICANT: Miller, Charles
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Miller, Charles
Trohernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
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Matches 93; Conserva
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APPLICANT:
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179 GFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGL- 237
                                                                                                                                                                                                                                                               ; Sequence 4, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
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Best Local Similarity 29.1%
Matches 88; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Boldog, Ference
ITILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 2.0402-251
CURRENT APPLICATION NUMBER: 60/262,892
PRIOR PILING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-04
PRIOR PLING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 WPFGSALCKLVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLV 111
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18.9%; Score 305; DB 6; Length 259;
Best Local Similarity 33.0%; Pred. No. 1.6e-22;
Matches 93; Conservative 49; Mismatches 84; Indels 56; Gaps
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                               Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
                                                                                                                                                                           Patturajan, Meera
Burgess, Cahterine
Eisen, Andrew
                                                                                                                                                                                                                                                                  Baumgartner, Jason
Shimkets, Richard
Gusev, Vladimir
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Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
                                                                                  Guo, Xiaojia
Zerhusen, Bryan
Andrew, David
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                                                                                                                                                           Mezes, Peter
                                                                                                                                                                                                                                                  folenc, Adam
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Casman,
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LENGTH: 259
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120 HPLRARGLRSPROAAAVCAVLWVLVIGS----LVARWLLGIQEGGFCF----RSTRHNF 170
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29.1%; Pred. No. 6.8e-22;
tive 54; Mismatches 128; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR; TITLE OF INVENTION: Protein a TITLE OF INVENTION: US-0456 CURRENT APPLICATION NUMBER: US/11/157,930 CURRENT APPLICATION NUMBER: US/09/828,478 PRIOR APPLICATION NUMBER: US/09/828,478 PRIOR FILING DATE: 2000-04-07 PRIOR PILING DATE: 2000-04-07 PRIOR PILING DATE: 2000-04-07 PRIOR FILING DATE: 2000-12-13 NUMBER: ESQ ID NOS: 16 SOFTWARE: PASICE OF US: 16 SOFTWARE: PASICE OF US: 16
                                                                                                      238 --TVRLAVGWNA-CALLETIRRALYITSKLSDANCCLDAICY 276
                                                                                                                                              218 LDTLCLSIIMSSTCELERVLPTALLVTLWLAYVNSCLNPIIY 259
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§ Sequence 6, Application US/11157930 
§ Publication No. US20050266482A1 
§ GENERAL INFORMATION: 
§ APPLICANT: Xiao, Yonghong 
§ TITLE OF INVENTION: Regulation of Human CyeLT2-Like GPCR 
§ TITLE OF INVENTION: Proceed 
§ FILE REFERENCE: 04974.00458
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SEQ ID NO 66
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APPLICANT: Hoffmann, Marcel
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT TILING DATE: 2005-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR PLING DATE: 2004-05-12
PRIOR PLING DATE: 2004-06-12
PRIOR PLING DATE: 2004-06-13
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 VSL---AVAFTFPFITTVTCYLLIIRSLRQ-----GLRVEKLKTKAVRMIAIVLAIFL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VADLCLLCTLPFVLHSLRDTSDTPL----CQLSQGIYLTNRYMSISLVTAIAVDRYVAVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 NSWRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVG----QAEATRKAARWWANLLVFV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCFLPLHVGLTV---RLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQ 284
                                                                                                                                                                                                                                                                                                                                                                         4 TYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLA
                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                               18.6%; Score 300; DB 7; Length 367; 29.1%; Pred. No. 7.4e-22; ive 54; Mismatches 128; Indels
CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR PILING DATE: 2000-04-09
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 46, Application US/11127877; Publication No. US20050287565A1
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 29.1 Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HA 335
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LENGTH: 373
                                                                                                                                                                                                                                                                 US-11-157-930-6
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Length 373;

Score 298.5; DB 7; Pred. No. 1.1e-21;

18.5**%**; 26.2**%**;

Query Match Best Local Similarity

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APPLICANT: Hoffmann, Marcal APPLICANT: Hoffmann, Marcal APPLICANT: Hoffmann, Marcal APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Mydde Beta Protein Production
FILE REPERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: 105/11/127,877
CURRENT APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NLAVADL-------CLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 NLVVTDLLVGLSLPTRFAVYYGARGCLRCAFPHVLG--------YFLNMHC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 SISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWULVIGSLVARWLLGIQEGGFC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                           105 SLVTAIAVDRYVAVRHPLRARGLRSPROAAAVCAVLWVLV---IGSLVARWLLGIQEGG- 160
                                                                                                                                                                                                                                                                                                              213
                                                                                                                                                                                                                                                                                                                                                                                                                              200 ITCYDITSDEYLRSYFIXSMCTIVAMFCVPLVLILGCYGLIVRALIYK---DLDNSPLRR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : : | | | | : : | | | : | | | KSIYLVIIVLTVPAVSYIPFHVMKTMNLFARLDFQTPAMCAFNDRVYATYQVTRGLASLN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILPLICICVORYLAIVRPEAPAACROPACARAVCAFVW-LAAGA-VILSVLGVTGSRPC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 FRSTRHNFNSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221
                                                                                                                                                                                                 104
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                                                                                     20 GPGSSWGNSTVASTAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 KAARMVWANILLVFVVCFLPLHVGLTVRLAVGWN-----ACALLETIRRALYITSKLSDAN
                                                                                                                                                                                                                                                                                                                                                                                              161 -FCFRSTRHNF-----NSMRFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR
                                                                                                                                                              49 MQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSD----TPLCQLSQGIYLTNRYMSI
                                                    GTYNTCGSSDLTWPPAI -----KLGF-YAYLG----VLLVLGLLLNSLALWVFCCR
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39;
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Indels
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18.4%; Score 297.5; DB 7;
Best Local Similarity 29.4%; Pred. No. 1.3e-21;
Matches 89; Conservative 42; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 CCLDAICYYYMAKBFQEASALAVAPRAKAHKSODSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 SCVDPILYFLAGDTFRR--RLSRATRKASRRSEANL 350
  Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 66, Application US/11127877; Publication No. US20050287565A1; GENERAL INFORMATION:
  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Merchiers, Pascal G.
     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-66
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completed: February 9, 2006, 01:21:41
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Job time: 11.5 secs
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TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 LPLLVMVICYSGILKTLIR----CRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLINT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AAAVCAVLWVL-VIGSLVARWLLGIQEGGFCFRSTRH------NFNSMRFPLLGFY 181
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NLLVFVVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAK 281
                                              246 VLIIFLVCFTPFHAR---QVAVALMPDMPHHTSLVVYHVAVTLSSLNSCMDPIVYCFVTS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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; Reducate 2, Application Wo. U32005026055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
GORRESPONDENCE ADDRESS:
GORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 PQEPPGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFR 305
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                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 523, Application US/10995561
; Publication No. US20050272054Al
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-10-995-561-523
                                                                                                                                                    282 EFQ 284
                                                                                                                                                                                                                      303 GPQ 305
                                                                                                                                                                                                                                                                                                                                                                              US-10-995-561-523
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US-11-068-686-2
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ORGANISM:
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75 FVLHSLRDTSD--TPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQ 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GVVTSVITWVVAVPASLPGIIFTRSQKRGLHYTCSSHFPYSQYQFWKNPQTLKIVILGLV 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AAAVCAVLWVL-VIGSLVARWLLGIQEGGFCFRSTRH------NFNSMRFPLLGFY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 LPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGL---T 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 PPLYSLVPIFGFVGNMLVILILIN-----CKRLKSMTD--IYLLMLAISDLFFLLTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 FQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGBKFR 305
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17.9%; Score 288.5; DB 7; Length :
Best Local Similarity 26.2%; Pred. No. 9.2e-21;
Matches 75; Conservative 62; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UTHEK INFORMATION: /= "88C amino acid sequence" SEQUENCE DESCRIPTION: SEQ ID NO: 2:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta B.
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: /= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:43; Search time 165 Seconds

(without alignments)

1321.262 Million cell updates/sec

Title: US-10-083-168-16
Ferfect score: 1614
Sequence: 1614
Sequence: 1614
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 SUMMARIES

		Description	ношо	рошо	homo	homo	homo	_		_	_	tetra	homo		рошо		_				-					Q4rfp7 tetraodon n	homo	рошо		Q8bmc0 mus musculu	Q4g072 rattus norv		Q9ep66 mus musculu
SUMMAKIES		ID	Q6FH18 HUMAN	GPR35 HUMAN	Q4ZFVZ HUMAN	Q6ZMP9 HUMAN	Q4 VBNS_HUMAN	GPR35 MOUSE	QSKU21_HUMAN	Q8CB97 MOUSE	Q8BS98 MOUSE	Q4TAH0_TETNG	Q502U9_HUMAN	P2RY9 HUMAN	Q6NSP5_HUMAN	Q8BKK1_MOUSE	Q8BLG2_MOUSE	Q4S8W3_TETNG	GPRSS HUMAN	Q8TDS4 HUMAN	P2RY5 CHICK	G109B_HUMAN	Q8NGE4_HUMAN	Q7ZZA4_BRARE	Q9WU09_RAT	Q4RFP7 TETNG	GPR92 HUMAN	QSKU18 HUMAN	P2RYS HUMAN	P2RY5 MOUSE	Q4G072 RAT	Q53FA0 HUMAN	O9EP66_MOUSE
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		Score	1608	1602	1602	1602	1597	1124	1124		1109	4				400	392	376.5	376	375.5	368.5	368.5	368.5	368	365.5	365	362	362	361.5	357.5	356	355.5	348.5
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			35;	Homo sapiens (Human) Rukarvota: Metazoa:			NCBI_TaxID=9606;	DE SEC	A., E	rt P., Kstrang	Submitted (JUN-2004)	SUBCELLULAR	SIMILARITY:	CK541/65;	GO:0001584;	GO:0007186;	Incerpro; 1FK0002/6; Pfam: PF00001: 7tm 1:	ν Дц	PS00237;			Simi 8;							•	
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LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
                            LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKEFQEASALAVAPRAKAHKS 300
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Marren C.N., Aronstam R.S., Sharma S.V.;

"cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Orphan receptor.

-!- FUNCTION: Orphan receptor.

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SUBCELCULAR LOCATION: Integral membrane protein (By similarity).

-!- SUBCIFICITY: Expressed in all adult and fetal tissues
examined, including pancreatic isslets and skeletal muscle, with
relatively higher levels in adult lung, small intestine, colon and
                                                                                                                                                                                                                                                                                                                                                                                                                Hômo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Evarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus.";
Nat. Genet. 26:163-175(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876; Horikawa Y., Oda N., Cox N.J., Li X., Otho-Melander M., Hara M., Hinokio Y., Lindner T.H., Mashima H., Schwarz P.B.H., Gel Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Spolonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J., Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.
MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095; O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R., Heng H.H.Q., Kolakowski L.F. Jr., George S.R.; "Discovery of three novel G-protein-coupled receptor genes."; Genomics 47:310-313(1998).
                                                                                                                                                                                                                                       GPR35 HUMAN STANDARD; PRT; 309 AA. Q9HC97; 043495; Q8GUH4; 16-OCT-2001 (Rel. 40, Created) 13-SEP-2005 (Rel. 48, Last sequence update) 17-SEP-2005 (Rel. 48, Last annotation update) Name=GPR35;
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EMBL; AP089087; AAG17965.1; -; mRNA.
EMBL; AY275467; AAP32299.1; -; Genomic_DNA.
Ensembl; ENSG00000178623; Homo sapiens.
HGNC; HGNC:4492; GPR35.
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Pfam, PF00001; 7tm 1; 1.

PROMING, PRO0237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRPEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Transducin coupled receptor; Glycoprotein; Polymorphism; Receptor; Transmembrane.

Transmembrane.

Extracellular (Potential).
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Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential).
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0; Mismatches 2: ---
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Extracellular (Potential).
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Extracellular (Potential).
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/FTId=VAR_013606.
A -> R (in_ Ref. 1).
97734FB7231B26F0 CRC64;
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
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'FTId=VAR_013605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTIG=VAR_013601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTId=VAR_013602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_013603.
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Matches 307; Conservative
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258
309
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Aypothetical protein FLJ16773
                                                                                                 NCBI_TaxID=9606;
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPSAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMAFPLLGF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR 240
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                                                                         Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NIAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
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99.3%; Score 1602; DB 2; Length 309;
Best Local Similarity 99.4%; Pred. No. 4.9e-112;
Matches 307; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                 Haakenson W., Trani L., Schatzkamer K.; "The sequence of Homo sapiens BAC clone RP11-27M15."; Submitted (JUN-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;
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Last annotation update)
        Last annotation update)
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QEZMP9;
        13-SEP-2005 (TrEMBLrel. 31 Hypothetical protein GPR35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane
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Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (OCT-2002)
                                                                 Homo sapiens (Human)
                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                                                        NCBI_TaxID=9606;
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YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARWWANLLVFVVCFLPLHVGLTVR 240
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      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.3%; Score 1602; DB 2; Length 3
99.4%; Pred. No. 6e-112;
ive 0; Mismatches 2; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4VBNS_HUMAN PRELIMINARY;
Q4VBNS;
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Matches 307; Conservative
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                                                                                        NUCLEOTIDE SEQUENCE.
Homo sapiens (Human)
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145 9

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TISSUE-G-protein coupled receptors;

WEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBENER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MIschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MIschenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

MA Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

MA Stapleton M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

MA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MIlalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Mannan A., Schain J.E., Jones E.J.M., Marra M.A.,

M. Schain J.E., Jones S.J.M., Marra M.A.,

M. Schain J.E., Jones S.J.M., Marra M.A.;

M. Schain J.E., Jones E. W., Marra M.A.,

M. Schain J.E., Jones E. W., Marra M.A.;

M. Schain J.E., Jones E. W., Marra M.A.;
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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-!- SUBCELLIULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; BC095500; AAH95500.1; -; mRNA.
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSTIE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSTIE; PS50262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches 306; Conservative
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                                                                                    TaxID=9606;
                                                                                                                                                                         NUCLEOTIDE
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STRAIN-ESTBL/63; TISSUE-MERMENT Gland,

KRAIN-ESTBL/64; TISSUE-MERMENT Gland,

KRAIN-ESTBL/65; PubMedel12477932; DOI=10.1073/pnas.242603899;

KRAIN-ESTBL/65; PubMedel12477932; DOI=10.1073/pnas.242603899;

KRAIN-ESTBL/65; Pelingold E.A., Grouse L.H., Derge J.G.,

KRAIN-ESTBL/65; Pelingold E.A., Grouse L.H., Derge J.G.,

KRAIN-ER, D.C., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechnis R.P., Jordan H., Moore T., Wars S.I., Wang J., Heiseh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., Male S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley W. Sodergen E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genetic variation in the gene encoding calpain-10 is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-- FUNCTION: Orphan receptor.
-- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
HIORIKAWA Y., Cda N., Cox N.J., Li X., Orho-Melander M., Hara M., Hinder T.H., Mashima H., Schwarz P.E.H., del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J., Paler L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF200349; AAG18487.1; -; mRNA.

EMBL; BC027429; AAH27429.1; -; mRNA.

Ensembl; ENSWUSG0000026271; Mus musculus.

MGI; MGI:1929509; Gpr35.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR00276; GPCR_Rhodpsn.

InterPro; IPR02286; P2_purnocptor.
  307 AA
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                                                                                                                    Probable G-protein coupled receptor 35.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01157; P2YPURNOCPTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes mellitus.
  STANDARD;
                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
GPR35_MOUSE
                                                                                                                                             Name=Gpr35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bell G.I.;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Matches 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRS-TRHNFNSMRFPLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAH 298
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Inoue S., Yoshida S., Urakawa I., Mizutani S., Okazaki H.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL, AB041940; BAD835941; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
Vlinked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
  Glycoprotein; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1124; DB 1; Length 307; Pred. No. 3e-76; Indels (1)
                                                                                                Cytoplasmic (Potential).
2 (Potential).
2 (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                             6 (Potential).
Extracellular (Potential)
7 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0B3D02CECB16710D CRC64;
                                                      Extracellular (Potential)
                                                                                                                                                                                                                                                                              5 (Potential).
Cytoplasmic (Potential).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%;
71.9%;
          receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor.
Name=KPG 007;
Homo saplens (Human).
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QSKU21;
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                               Transmembrane
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                            .; IEA
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-OCT-2003 (TYEMBLREL. 25, Last annotation update)
Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830121M19 product:G protein-coupled receptor 35, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFYLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEALN=CS7BL/6J; TISSUB=Bone;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carnino1 P., Hayashlaski Y.;
"High-efficiency full-langth cDNA cloning.";
"High-efficiency full-langth cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CS7BL/6J; TISSUE=Bone;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; P801157; PZYPURNOCTR.
PROSITE; P800237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-protein coupled G-protein Receptor; Transducer; Transmembrane.
SEQUENCE 307 Aa; 34152 MM; 0B3D02CECB16710D CRC64;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0045028; P:purinergic nucleotide receptor activity, G-.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; P:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR002286; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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71.9%; Pred. No. 3e-76;
iive 30; Mismatches 5
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Q8CB97;
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Ksaukwa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Wilming L., Wannahaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

R EMBL, AGASSOS, MAT. MAT. P., MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Bone; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nomalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Shibmata K., ITSSUB-Bone;

Shibmata K., Itoh M., Aizawa K., Nagada, S., Sasaki N., Carninci P.,

Shibmata K., Itoh M., Aizawa K., Nagada, S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RIKEN integrated sequence analysis (RISA) system-384-format

Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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GO, GO:0016021; C:integral to membrane; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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STRAIN=C57BL/6J; TISSUE=Bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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InterPro; IPR002286; F2_ Pfam; PF00001; 7tm_1; 1_

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TISSUB-Embryonic body between diaphragm region and neck;
MEDLINE-21085660, PubMed=11217851, DOI=10.1038/35055500,
Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gasakerland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
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                                                                                                                                                                                                                                                            1 MNST--TCNST-LTWPASVNNPPTIYSALLLVLGLLLINSVALWVFCYRWHQWTETRIYMT
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TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                            Gaps
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430051L15 product:G protein-coupled receptor 35, full insert sequence.
                                                                                                                                                                                            9
                                                                                       Transmembrane
                                                                                                                                              Query Match 69.6%; Score 1123; DB 2; Length 307; Best Local Similarity 71.9%; Pred. No. 3.6e-76; Matches 223; Conservative 30; Mismatches 51; Indels
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01157; P2YPUNNOCPTR.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS0262; G PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Receptor; Trans SEQUENCE 307 AA; 34140 MW; 8E8439AAED5F7656 CRC64;
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"High-efficiency full-length cDNA cloning.";
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01-WAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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QBBS98_MOUSE PRELIMINARY;
QBBS98;
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TISSUE=ES7BL/6J;

C TISSUE=Embryonic body between diaphragm region and neck;

TISSUE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yamamoto R., Tawa M., Ohara E., Watshiki M., A Pujiwake S., Inoue K., Togawa Y., Tawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Embryonic body between diaphragm region and neck;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Saro K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J;
TISSUE=Embryonic body between diaphragm region and neck;
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GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
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PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                   Nature 409:685-690(2001).
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NUCLECTIDE SEQUENCE.

NUCLECTIC SET SET SET SET SET SET SECTION S., SEGUENCE SET, SEGUENCE S., SEGUENCE S.,
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SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation sequence. (Fragment).
13-SEP-2005 (Fragment).
13-SEP-2005 (Fragment).
14-Tetraodon nigroviridis (Green puffer).
15-Tetraodontides; Tetraodontiformes;
15-Tetraodontides; Tetraodontiformes;
15-Tetraodontides; Tetraodontiformes;
15-Tetraodontides;
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                           Transmembrane
                                                                                                                                                                                                                                  . 9
                                                                                                                                              / Match 68.7%; Score 1109; DB 2; Length 307; Local Similarity 71.3%; Pred. No. 4e-75; les 221; Conservative 30; Mismatches 53; Indels e
                                                                           CRC64;
                                           Transducer;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer
SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC
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Nature 431:946-957(2004).
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Q4TAHO;
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NIH MGC Project;
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MEDLINE=22388257; PubMeda12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., McGran D.M., Soderstan R.J., Malek J.A., Gunaratne P.H.,

Villalon D.K., Muzny D.M., Sodersen B., Lu, X., Gibbs R.A.,

A Rahay J., Helton R., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
-i- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. Babl; CARASO100735; CAF90112.1, -j Genomic_DNA. InterPro, IPR000276; GPGR Rhodpsn. InterPro, IPR002169; P2Y5_purnocptor.
                                                                                                                                   Pfam; PF00001; 7tm 1; 1.

PRINTS; PR0237; GPCRRHODOPSN.
PRINTS; PR01067; P2YSORPHARR.
PROSITE; PS05027; GPCRENTRRCEP_F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                           305 AA; 34283 MW; E9F740AD3FF04F32 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Matches 106, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                              NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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050209
DE UGF021
DE UGF02
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44 AVYSVVPILGLITNSVSLFVPCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 WILVLSGGISASLFSTTNVNNATTTCPEGFSKRVWKTYLSKITIFIEVVGFIIPLILNVS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 CSSVVIRTL--RKPATLSQVGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQRASALAVAPRAKAHKSQDSLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butrerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 -DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AYLGULLUGLLINSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR ENGRANCY.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL, BC095538; Ash95538, 1; -; mRNA.
Ensembl; ENSG0000147145; Homo sapiens.
InterPro; IPR000188; P2Y5_purnocptor.
PF00001; 7fm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.0%; Score 403; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.5e-22;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (G-protein coupled
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MEDLINE=97225799; PubMed=9073069; DOI=10.1016/S0378-1119(96)00722-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO1067; P2Y5ORPHANR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Trans SEQUENCE 370 AA; 41881 MW; 38267561B1029E48 CRC64;
                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P2RY9 HUMAN STANDARD; PRT; 370 AA. 099677; O1512; O10-1NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 107-MAY-2005 (Rel. 47, Last annotation update) 12Y purincoeptor 9 (P2Y9) (Purinergic receptor 9) receptor GPR23) (P2X5-1ike receptor).
                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE.
TISSUE=G-protein coupled receptors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=GPR23; Synonyms=P2RY9;
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10;

ROLOGO BF. WARWART T. JUNGE R.P. WESTERS A. Cheng R. Heng H.H.O. ROLAGOWERLI L.F. June 19. No. 19. No.

EMBL; U66578; AAAC51301.1; -; Genomic_DNA.

EMBL; U90323; AAB62087.1; -; Genomic_DNA.

EMBL; U90323; AAB62088.1; -; mRNA.

EMBL; AF005419; AAB66322.1; -; Genomic_DNA.

EMBL; AF005419; AAB66322.1; -; Genomic_DNA.

EMBL; AV590083; CAD18851.1; -; Genomic_DNA.

EMBL; AL590083; CAD18851.1; -; Genomic_DNA.

EMBL; AL500083; CAD18851.1; -; mRNA.

EMBL; AU50000147145; Homo sapiens.

BRSP; P34996; 1DDD.

Ensembl; ENSC00000147145; Homo sapiens.

BRC; HGNC; HGNC:4478; GFR23.

MIN; 300086; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

GO; GO:0004930; F:G-protein coupled receptor protein signalin. ..; TAS.

InterPro; IPR001276; GPCR_Rhodpsn.

EnterPro; IPR001276; P2FCpurocptor.

EMBL; U90323; P275_purnocptor. MEDINES-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

MEDINES-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

MISCAULS E.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Anatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimmood J.W., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimmood J.W., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not hippocampus. SIMILARITY: Belongs to the G-protein coupled receptor 1 family. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Not detected in the brain regions thalamus, putamen, caudate, frontal cortex, pons, hypothalamus and PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane. Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A., Lehrach H., Maindl A., Minx P.J., Hillier L.W., Willard H.F., Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A., Relson D.L., Wainstock G., Sulston J.E., Durbin R., Hubbard T., Gibbs R.A., Beck S., Rogers J., Bentley D.R.; "The DNA sequence of the human X chromosome."; Nature 434:325-337(2005). 2 (Potential). Extracellular (Potential). 3 (Potential). Extracellular (Potential)
1 (Potential). Cytoplasmic (Potential).
2 (Potential). NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR01067; P2Y5ORPHANR. and mouse cDNA sequences." 43 64 73 94 112 133 TOPO DOM TRANSMEM TOPO DOM TRANSMEM TOPO DOM TRANSMEM removed. 

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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 -DTSDTFLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 WPFGDT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 TNCFLERPAKIMYPITLCLATINCCFDPPIYYFTLESFQKSFYI-----NAHIRMESLF 334
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.

TISSUB=PCR rescued clones;

TISSUB=PCR rescued clones;

TISSUB=PCR rescued clones;

Strausbers;

Rubinel=218955;

Fubmed=12477932;

Foruse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AYLGVLLVLGLLLNSLALWVPCCRMQQWTETRIYMTNLAVADLCLLCTLPF-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                             (Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.9%; Score 402; DB 1; Length 370; 34.1%; Pred. No. 4.1e-22;
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F -> L (in Ref. 3).
20857F52A3929E48 CRC64;
                                          4 (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                           Extracellular (Potential)
                                                                                                               5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
                                                                                                                                                                                                                                                              7 (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (IN-linked (GlCNAC. .) (IN-lin
       (Potential)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
G protein-coupled receptor 23.
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370 AA;
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44 AVYSVAFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
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Director MGC Project;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Li-SubELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL; BC069996; AAH6996.1; -; mANA.

RO; GO:0016021; C:integral to membrane; IEA.

RO; GO:0016021; F:integral to membrane; IEA.

RO; GO:0004872; F:receptor activity; IEA.

RO; GO:0004872; F:receptor activity; IEA.

RO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

RO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

RO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

RO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

RO; GO:0007186; P:RN00276; GPCR Modpsn.

RICEPPO; IRR00237; GPCR MODPSN.

PRINTS; PRO1007; PX5ORPHANR.

RRINTS; PRO1007; PX5ORPHANR.

RROSITE; PS00237; GPROTEIN RECEP FI 1; UNKNOWN 1.

RROSITE; PS00227; GPROTEIN RECEP FI 2; 1.

ROSITE; PS00226; GPROTEIN RECEP FI 2; 1.

ROSITE; PS00226; GPROTEIN RECEP FI 2; 1.

ROSITE; PS00227; GPROTEIN RECEP FI 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        · · ; IEA
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield X.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schentch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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QBEKKI;
QBEKKI;
O1-MAR-2003 (TrEWBLrel. 23, Last sequence update)
O1-MAR-2004 (TrEWBLrel. 26, Last annotation update)
O1-MAR-2004 (TrEWBLrel. 26, Last annotation update)
MUS musculus 12 days embryo spinal aganglion cDNA, RIKEN full-length
enriched library, clone:10130067B12 product:P2Y PURINOCEPTOR 9, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 103; Conservative
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CENTENCINE SEQUENCE.

NELLOLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

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Nymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Nymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Spinal ganglion; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                      STRAIN=CSTBL/6J; TISSUE=Spinal ganglion; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Rayashizaki Y.; Hajashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Spinal ganglion; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                                                               Muridae; Murinae; Mus.
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63 AVADICILCTIPF-VLHSLR---DISDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAV 118
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor protein signalin. . .; IEA.

GO; GO:0007186; F:signal transduction; IEA.

InterPro; IPR00276; GPCR Rhodopsn.

InterPro; IPR002188; P2Y5_purnocptor.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
24.8%; Score 400; DB 2; Length 370;
Best Local Similarity 34.3%; Pred. No. 5.8e-22;
Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sanoth H., Sakai C., Sakai K., Sakazume N., Sono H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T. Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDB/databases.
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
MADS musculus 9.5 days embryo parthenogenote cDNA, RIXEN full-length
enriched library, clone:Bl30055L15 product:P2Y PURINOCEPTOR 9, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41956 MW; AB126B42343AE6E1 CRC64;
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01067; P2Y5ORPHANR.
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                                                                                                                                                                                                                                                                                             STRAIN-CSTBL/63 PubMed=11217851; DOI=10.1038/3505500;
X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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STRAIN=2CS/BL/6J; TISSUB=Parthenogenote;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Sequencing pipeline with 384 multicapillary sequencer.";
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
                                                                                         STRAIN-C57BL/6J; TISSUE-Parthenogenote;
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NCBI_TaxID=10090,
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104 WPFGDT-LCKISGTAPLTNIYGSMLPLTCISVDRFLAIVYPFRSRTIFTRRNSAIVCAGV 162
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:purinergic nucleotide receptor activity, G-. .; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR000276; GPCR Rhodpsn.

InterPro; IPR000188; P2Y5_purnocptor.
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Togawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases -- I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity). EMBL, AKO45289; BAC32299.; -, MUR musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 WILVLSGGISASLPSTTNVNNATTTCFEGFSKRVWKTYLSKITIFIEVVGFIIPLINVS
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PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transducer; Transmembrane.
SEQUENCE 370 AA; 41872 MM; 084C79FEDPD32050 CRC64;
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PRINTS; PR01067; P2Y5ORPHANR.
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1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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2443163 Notal number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abg95172 Human GPC	Human	Abg95159 Human GPC	Abp82002 Human G p	Human	4 Human	Ado78094 Human GPR	Human	Aeb15039 Human GPR	6	1 Orphar	Human	Human	Human	Ado78095 Human GPR	Adr10454 Human pro		Ado29395 Mouse GPC	7 Human	Human	Abg73513 Human p2y	Abp81870 Human G p	Human	Adf91778 Human P2Y
OI OI	ABG95172	AAY79576	ABG95159	ABP82002	ADB67656	AD029394	AD078094	ADV73203	AEB15039	AAY69989	ADF70461	ADF50511	AAY58645	ADA84069	AD078095	ADR10454	ADP29765	AD029395	AAW62597	ABP61511	ABG73513	ABP81870	ADH69286	ADF91778
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Query Match	100.0	99.6	99.6	99.6	99.6	99.6	9.66	9.66	9.66	99.3	99.3	99.1	98.9	98.9	98.9	98.9	85.3	69.5	24.8	24.8	24.8	24.8	24.8	24.8
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ADO29049	ADQ81575	ADS84260	ADV35123	ADF70491	ADH69285	ADF91777	AD029050	ABP61510	ADS84259	AD029415	ADW44804	ADW44778	AEB20962	ADW44818	ADW44796	ADW44807	ADW44802	ADW44810	ADW44805
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## ALIGNMENTS

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor; mutant; mutein. Leonard JN; Behan DP, Maciejewski-Lenior D, ABG95172 standard; protein; 309 AA. Human GPCR GPR35 mutant A216K. 26-FEB-2002; 2002WO-US005625. 26-FEB-2001; 2001US-0271913P. (first entry) (AREN-) ARENA PHARM INC. Chalmers DT, WPI; 2002-706980/76. WO200268600-A2. Homo sapiens 06-SEP-2002. 04-DEC-2002 Synthetic. ABG95172; Lin I, Liaw RESULT 1 ABG95172 ID ABG95 

New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. N-PSDB; ABS73401

Example 2; Page 189-190; 201pp; English.

The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polymuclectide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension,

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reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hypertylasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhintis, and angina. The present sequence represents a mutant human GPCR
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                                                                                                                                                           Length 309;
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                                                                                                                                                           100.0%; Score 1615; DB 5; 100.0%; Pred. No. 2.6e-168;
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(TEXA ) UNIV OF TEXAS SYSTEM
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Bell GI, COX NJ;
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Matches 309; Conservative
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                                                                                                                       Sequence 309 AA;
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13-MAY-1999;
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Hanis CL, B
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The present sequence is that of the human gene encoding G protein coupled receptor, GPR35 as deduced from a composite CDNA (see AAA27485). The sequence of GPR35 as deduced from a composite CDNA (see AAA27485). The sequence of GPR35 is similar to that of a putative purinoceptor P279 (34.1% identity) suggesting that ATP or other nuclectide is its ligand. GPR35 mRNA was detected in all adult and foetal tissues examined with relatively higher levels in adult lung, snall intestine, colon and camach. In these tissues, there are 2 major transcripts of 2.4 and 4.4 kb, whereas in skeletal muscle there is a single transcript of 9.4 kb. The GRSS gene is located in a 49,136 bp region (see AAA2745) within the CNIDDAI region of human chromosome 2. This region also includes the CAPN10 gene, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CAPN10 gene are responsible for a usecptibility to type 2 diabetes. Claimed methods for screening for a compensity for type 2 diabetes mellitus are based on detection of a polymorphism in a calpain encoding nucleic acid. Methods are also claimed for identifying modulators of calpain activity, and using these contains to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport
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                                                                                                                 Method for screening for type 2 diabetes mellitus comprises detecting polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.
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Pred. No. 1.2e-167;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                Claim 75; Page 237-238; 257pp; English.
WPI; 2000-339702/29.
N-PSDB; AAA2748S, AAY79574, AAY79576.
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Best Local Similarity 99.7%;
Matches 308; Conservative
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                                                                                                                                                                                                                                                                                                                                                    , human G-protein coupled receptor (GPCR), useful for screening agonist inverse agonist compounds for treating diseases associated with GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating classes associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI) stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present
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myocardial infarction; MI; stroke; glaucoma; anxiety;
prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
prostatic hypertrophy; receptor.
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                                                                                                                                                                                                                                                          Chalmers DT, Behan DP, Maciejewski-Lenior D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents an endogenous human GPCR
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                                                                                                                                                              26-FEB-2002; 2002WO-US005625.
                                                                                                                                                                                            26-FEB-2001; 2001US-0271913P.
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Best Local Similarity 99.7
Matches 308; Conservative
                                                                                                                                                                                                                             (AREN-) ARENA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                         New human G-protein
                                                                                                                                                                                                                                                                                                          WPI; 2002-706980/76
                                                                                                                                                                                                                                                                          Ortuno D;
                                                                                                                                                                                                                                                                                                                            N-PSDB; ABS73345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 309 AA;
                                                                                                WO200268600-A2
                                                                    sapiens
                                                                                                                                36-SEP-2002.
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                                                                    Homo
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino cardids. Also described: (1) an assay for the detection of a particular GCC acids. Also described: (1) an assay for the detection of a particular GCC and (2) an isolated antibody having high specificity and high affinity or aridity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. and in the production of specific antibody against a particular GPCR. and in the production of specific antibody against a particular GPCR. and in the production of specific cartibods and antibodies and antibodies are also useful for disposing and designing the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disposing and designing drugs for treating immune-related diseases, immunological-related cell proliferative ciseases, or autoimmune diseases, growth-related diseases, concertions, allergies, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, concertions and acute inflammation, allergies, Crohm's disease, glabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, concertions and scute concernation, renal disorders, rheumatoid arthritis, trauma, ulcers, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders, rheumatoid arthritis, the angely of the and the disorders and acute involved. The antibodies may be and the disorders and acute involved. The antibodies may be and the disorders and acute involved. The antibodies and part of the actions of the actions of the actions of the actions of the and provides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                       G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; grotein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Altaeimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; paoriasis; anxiety; depressaon; schizophremia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; tramma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the
                                                                                                                                                                                    protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
                                                                                                                                Human G protein-coupled receptor GPR35 protein SEQ ID NO:492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2000; 2000US-0257144P.
                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases.
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                                                                                04-MAR-2003
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                            ABP82002;
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Length 309;

Score 1609; DB 6; Pred. No. 1.2e-167;

99.68;

Query Match Best Local Similarity

ABP82002 standard; protein; 309 AA.

RESULT 4
ABP82002
ID ABP8

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Gaps ö

Indels

Pred. No. 1.2e-167; 0; Mismatches 1;

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180 240 240

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61 NIAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                            61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                           121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
                                                                                                                                                                                                                                                                                                                                 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBFQBASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                          241 LAVGWNACALLETIRRALYITSKUSDANCCLDAICYYYMAKBFQBASALAVAPRAKAHKS 300
                                                                         1 MNGTYNICGSSDLIWPPAIKLGFYAYLGVLLVGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                             181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                                                                                    181 YLPLAVVVFCSLKVVTALAQRPPTDVGQARATRKAARNVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                                                                                                121 PLRARGERSPRQAAAVCAVLWVLVIGSLVARWLLGIOGGGGCFRSTRHNFNSMRFPLLGF
                                                   1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQOWTETRIYMT
 99.78;
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                   Matches 308; Conservative
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   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PRIM-) PRIMAL INC.
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                                                                                                     61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                       61 NLAVADLCLLCTLPFVILHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
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                                                                                                                                                                                                                                         YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRMVWANLLVFVVCFLPLHVGLTVR 240
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                                                                                                                                                                       121 PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                  1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                              181 YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAARMVWANLLVFVVCFLPLHVGLTVR
                                1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
 Gaps
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Koishi R, Nakamaru K;
 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G protein-coupled receptor 35, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardiant, Gene therapy; heart failure; human; G protein-coupled receptor 35; receptor.
 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB67656 standard; protein; 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002; 2002JP-00054388.
15-APR-2002; 2002JP-00112228.
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Matches 308; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-679959/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
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Transpent coupled receptor; GPCR; drug screening; diagnosis; transpent mouse; neurological disorder; adrenal gland disorder; cardiovascular disorder; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; immune disorder; bone disorder; blood disorder; immune disorder; bone disorder; disorder; broad disorder; metabolic disorder; immunitive disorder; cancer; widney disorder; uterus disorder; prostate disorder; persit disorder; scancer; which disorder; thomach disorder; pancreas disorder; spleen disorder; thymus disorder; prostate disorder; spleen disorder; which disorder; pancreas disorder; spleen disorder; cancing a string disorder; antidiarkhythmic; contral nervous system; respiratory; antidiarrhoelc; antidiabetic; wirucide; hepatocropic; antibacterial; antidansemic; antidiabetic; wirucide; hepatocropic; antibacterial; antidialergic; antidiabetic; mimmunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; mimunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li F;
Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J,
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
ADO29394 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                     Human GPCR GPR35, SEQ ID NO:496.
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N-PSDB; ADO29916.
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Length 309

DB 7;

99.6%; Score 1609;

Sequence 309 AA;

Query Match

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

(first entry)

26-AUG-2004

ADO78094;

Claim 151; SEQ ID NO 496; 542pp; English

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of sequences at least 90% identical to the GPCR proteins and nucleic acids of sequences at least 90% identical to the GPCR proteins and nucleic acids of associated with GPCRs of the invention; methods of screening for associated with GPCRs of the invention or a comprising a GPCR gene of the invention is a mouse comprising a GPCR gene of the invention and second which has transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has comprising a GPCR gene of the invention and kits comprising comprising a GPCR gene of the invention. The comprising a GPCR nucleic acids and proteins may comprising a conformation of a disease or schizophrenia; alsorders of the adrenal gland; disorders (e.g., Alzheimer's disease, disease, disease or schizophrenia; comporation, diabetic neuropathy, Parkinson's disease or schizophrenia; comporated infraction); muscular disorders (e.g., angina, cardiac arrhythmia or mycardial infraction); muscular disorders (e.g., angina, cardiac arrhythmia or comporated infraction); muscular disorders (e.g., auchimmune disorders) and disorders of the kidney, liver, lung, broaste, over, or the primee appe electronic format directly from WIPO at frp.wipo.int/pub/published_pct_sequences.

Sequence 309 AA;

ö 120 300 240 240 9 9 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTBTRIXMT 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR Gaps ö 99.6%; Score 1609; DB 8; Length 309; 99.7%; Pred. No. 1.2e-167; 1; Indels 0; Mismatches Matches 308; Conservative ODSLCVTLA 309 Query Match Best Local Similarity 241 181 61 181 301 셤 셤 δ 요 ð g ò 셤 δ ò

agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and sequence of a human GPR35. tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; prostate cancer; colon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; GPR35. Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring. The invention relates to pharmaceutical compositions that comprise an Claim 72; SEQ ID NO 9; 124pp; German Koslowski M; 22-NOV-2002; 2002DE-01054601. 22-NOV-2002; 2002DE-01054601 (GANY-) GANYMED PHARM Sahin U, WPI; 2004-421820/40. N-PSDB; ADO78086 DE10254601-A1 Homo sapiens 03-JUN-2004 Human GPR35 Tuereci O, 

ö 120 120 YLPLAVVVECSLKVVTALAQRPPTDVGQABATRKAKRMVWANLLVFVVCFLPLHVGLTVR 240 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300 9 1 MIGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTFTRIYMT NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH Gaps ö Length 309; Indels ï Score 1609; DB 8; Pred. No. 1.2e-167; 0; Mismatches 1; 99.6%; Best Local Similarity 99.7 Matches 308; Conservative 61 121 121 241 181 Query Match 쇰 Š 음 ઠે 윱 ð 셤 ઠ

Sequence 309 AA;

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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKEFQEASALAVAPRAKAHKS 300

ODSLCVTLA 309

301

ADO78094 standard; protein; 309 AA.

RESULT 7 ADO78094 ID ADO7

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301 QDSLCVTLA 309

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LAVGWNACALLETIRRALYITSKISDANCCLDAICYYYMAKEPQRASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 YLPLAVVVPCSLKVVTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCFLPLHVGLTVR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents the amno acid sequence of a protein upregulated in human colon cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIGHTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRWQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 309;
                                                                                                                                                                                                                                                                                                                                                                    Head RD, Hippenmeyer PJ, Klein BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                      Human colon tumor cell upregulated protein SEQ ID NO 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%; Score 1609; DB 9;
99.7%; Pred. No. 1.2e-167;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 44; 257pp; English.
                            ADV73203 standard; protein; 309 AA.
                                                                                                                                                       cancer; neoplasm; cytostatic.
                                                                                                                                                                                                                                                                          28-OCT-2003, 2003WO-US034019.
                                                                                                                                                                                                                                                                                                       29-OCT-2002; 2002US-0422176P
                                                                                                                                                                                                                                                                                                                                                                    Bourner MJ, Bu JJ, Head 1
Mazzarella RA, Staten NR;
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                     (PHAA ) PHARMACIA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-039958/04.
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                                                                                                                                                                                                                WO2004110345-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 309 AA;
                                                                                                                                                                                  Homo sapiens
                                                                                         10-MAR-2005
                                                                                                                                                                                                                                              23-DEC-2004.
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                                                          ADV73203;
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The invention relates to the use of human G-protein coupled receptor 35 (GPR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The therapeutic agents are screened by contacting a test compound with GPR35 polymetried, and detecting the binding of the test compound with GPR35 polymetried diseases in a mammal, comprising determining the amount of the GR835 polymuclectide in a sample taken from the mammal, and determining the amount of the GR835 polymuclectide in healthy and/or diseased mammals (C GR835 polymetried). Or or treating the above specified diseases in the mammal, comprising a therapeutic agent that binds to the GR835 polymetried; 30 use of regulators of a GR835 for the preparation of the pharmaceutical composition or for the regulation of GR835 regulator, determining whether the regulation amount of the pharmaceutical composition or for the regulator ameliorates the compliance of the above specified diseases; and (4) a method for the symptoms of the above specified diseases; and combining the regulator with an acceptable pharmaceutical composition; comprising useful for symptoms of the above specified diseases in a mammal, and combining the regulator with an acceptable pharmaceutical cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, and agastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders in a mammal, e.g. humans (preferably), dogs, cats, cows, horses, rabbite, and monkeys. This sequence represents human GPR35.
                                                                                                                                                                                                                                                                                                                                               G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR; screaning; cardiovascular disease; gastrointestinal disease; liver disease; cancer; neoplasm; metabolic disorder; hematological disease; respiratory disease; inflammation; hematological disease; respiratory disease; inflammation; gastrointestinal-gen.; hepatotropic; cardiovascular-gen.; respiratory-gen.; espiratory-gen.; espiratory-gen.; respiratory-gen.; hepatotropic; cytostatic; metabolic; antianemic; respiratory-gen.; antiinflammatory; neuroprotective; uropathic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 2; 96pp, English.
                                                                                                                                                 AEB15039 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                 08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                    Human GPR35 polypeptide.
301 QDSLCVTLA 309
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                                                                                                                    NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                    180
                                                                           NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                                                                 PLRARGLRSPROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                    121 PLRARGLRSPRQAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
                                                                                                                                                                                         YLPLAVVVFCSLKVVTALAQRPPTDVGQABATRKAKRMVWANLLVFVVCFLPLHVGLTVR
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                                                              1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor-associated protein; HRAP; Incyte clone 3083742;
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                      Length 309;
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                                          Indels
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238
/note= "Potential phosphorylation site"
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/label= Signature_sequence
/note= "G-protein_coupled_receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Potential phosphorylation
                      99.6%; Score 1609; DB 9; 99.7%; Pred. No. 1.2e-167;
                                Pred. No. 1.26
0; Mismatches
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                                           Matches 308; Conservative
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                                Similarity
  Sequence 309 AA;
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Modified-site
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                       Query Match
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The present sequence is human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUNO1 cDNA library. This sequence is expressed in haemacropoietic/immune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antianflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiantemic, antiantentic, antiantemic, antiantemic, antiantemic, antiantemic, antiantemic, antiantemic, antiantemic, autidiapetic, dematological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
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                                                                                   /note= "Potential phosphorylation site"
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      /note= "Potential phosphorylation
261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 76; 99pp; English.
                                                                                                                                                                                                                                                                                                                          98US-0160065P.
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Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman JL, Yue H, L
Corley NC, Baughn MR;
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N-PSDB; AAZ50891.
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                                                                                                                                                 WO200008155-A2
Modified-site
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                                                                                                                                                                                                                                                                   06-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPPU or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformation of cells with a fusion protein of an orphan receptor protein with a fluorescent protein useful for identification of ligands
                                                                                                                                                                                                                     ligand, orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP; GFPuv; Enhanced GFP; EGFP; human.
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                                                                                                                                                                            Orphan receptor ligand-related human protein SeqID84.
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Pred. No. 1.1e-166;
0; Mismatches 2;
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                                               ADF70461 standard; protein; 547 AA.
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23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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Best Local Similarity 99.4%;
Matches 307; Conservative
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                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the orphan receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-697654/66
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                                                                                                                                   12-FEB-2004
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                                                                                        ADF70461;
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RESULT 11
ADF70461
ID ADF70461
XX ADF70
XX ADF70
XX I 12-FE
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XX HOMO
XX Y 22-FE
PR 21-FF
XX Z 21-FF
XX Z Z -FF
PR 22-FF
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241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunitomo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; mutein; transformation; endocrine cell line;
expression cloning system; bioactive peptide; GPCR ligand; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshizawa M, Kishimoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Asp substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 24; SEQ ID NO 191; 316pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GPCR GPR35 D113A mutein (SeqID 191).
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                                                                                                                                                                                                                                                                                                                                                      ADF50511 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2003; 2003WO-JP004840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                        301 ODSLCVTLA 309
                                                                                                                                                     301 ODSLCVTLA 309
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Nishi T, Obinata M;
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                                       120
MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT 60
                                                                                                                                                                                                                                                                                                                           GPR35A; human; G-protein coupled receptor; purinergic; 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic; cytostatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian; hypotensive; hypotensive; hypotensive; hypotensive; cardiant; cerebroprotective; antinlcer; antiallergic; antimigraine; antidemetic; tranquillizer; antidepressant; neuroleptic; nootropic; anticonvulsant; therapy; diagnosis; vaccine.
                               NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH
                                                                                                   YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVGLTVR
                                                                                                                                          LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKBPQBASALAVAPRAKAHKS
                                                           PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.
                                                                                                                                                                                                                                                                                                                  Human G-protein coupled receptor GPR35A.
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                                                                                                                                                                                                                                                                                              (first entry
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N-PSDB; AAZ35390.
                                                                                                                                                                                   QDSLCVTLA
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              failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation; and dyskinesias such as Huntingdon's or Gilles de la Tourette's syndrome. The polypeptide is also useful for production of vaccines
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obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
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                                                                                                                                                                                                                                               Length 309;
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                                                                                                                                                                                                                                               Score 1597; DB 3;
Pred. No. 2.5e-166;
0; Mismatches 3;
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22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
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99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                         Best Local Similarity 99.0
Matches 306; Conservative
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N-PSDB; ADA84068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GPR35 protein.
                                                                                                                                                                                                            Sequence 309 AA;
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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTS expressed in normal tissue to phenotype/cell type of interest with all ESTS expressed in the phenotype/cell type of interest is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably care mumour The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell, and for regulating or cancer in a human, for detecting a tumour cell, and for regulating or tumour-associated markers. A polypeptide of the invention is useful so the immunogen for vaccinating an animal. The present sequence represents a tumour-associated antigen of the invention.
Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                               Claim 29; Page 448-449; 516pp; English.
                                                                                         cissue.
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## Sequence 309 AA;

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300
                                                                                                        61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                          61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH 120
                                                                                                                                                           121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
                                                                                                                                                                          240
                                                                                                                                                                                                                                                                 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300
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                                                                     1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWYFCCRMQQWTETRIYMT
                                                       MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVPCCRMQQWTBTRIYMT
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                                Gaps
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     Length 309;
                              3; Indels
    Score 1597; DB 6;
Pred. No. 2.5e-166;
0; Mismatches 3;
     98.94;
Query Match
Best Local Similarity 99.0
Matches 306; Conservative
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tumour-associated antigen; TAg; cancer; lung cancer; breast cancer; profette cancer; calon cancer; stomach cancer; pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human; 08735.
                          ADO78095 standard; protein; 394 AA
                                                                               (first entry)
                                                                                                          Human GPR35 isoform
                                                                              26-AUG-2004
                                                     ADO78095;
RESULT 15
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The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAg) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAg, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAg, or related nucleic acid, antibodies or host cells, are also useful for diagnosis and sequence of a human GPR35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWILGIQEGGFCFRSTRHNFNSMRFPLILGF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                        Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related compositions for diagnosis and monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQOWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 MIGTYNTCGSSDLTWPPAIXLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTALAVDRYVAVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMAFPLLGF
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Pred. No. 3.3e-166;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                         Claim 72; SEQ ID NO 10; 124pp; German.
                                                                                                                                                                                              Koslowski M;
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                                                                                               22-NOV-2002; 2002DE-01054601
                                                                                                                              22-NOV-2002; 2002DE-01054601.
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                                                                                                                                                              (GANY-) GANYMED PHARM AG
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Job time: 215.5 secs
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                              DE10254601-A1
   Homo sapiens.
                                                               03-JUN-2004.
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Sequence 20, Appl
Sequence 2, Appli
Sequence 159, App
Sequence 36, Appl
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8, Appli
30, Appl
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157, App
139, App
83, Appl
17, Appl
                                                           9, 2006, 01:00:39; Search time 33.5 Seconds (without alignments) 762.591 Million cell updates/sec
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                                                                                                                          1 MNGTYNTCGSSDLTWPPAIK......AVAPRAKAHKSQDSLCVTLA 309
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd
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1. /GgDZ_6/ptodata/1/iaa/5_COMB.pep:*

2. /GgDZ_6/ptodata/1/iaa/6_COMB.pep:*

3. /GgDZ_6/ptodata/1/iaa/H_COMB.pep:*

4. /GgDZ_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /GgDZ_6/ptodata/1/iaa/RE_COMB.pep:*

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US-10-314-048A-159

US-10-314-048A-36

US-09-170-496D-108

US-09-170-496D-222

US-09-944-807-21

US-10-314-048A-135

US-08-467-948A-8

US-08-467-948A-8

US-08-467-948A-8

US-08-467-948A-137

US-10-314-048A-137

US-10-314-048A-137

US-10-314-048A-139

US-09-745-842-17

US-09-745-842-17

US-09-10-745-842-17

US-10-314-048A-139

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US-09-10-745-842-17
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S-08-513-974B-374
S-10-314-048A-151
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5-09-745-842-15
5-09-979-603-2
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                                                                                                                                                                            572060 segs, 82675679 residues
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Gapop 10.0 , Gapext 0.5
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1614
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Score, Match
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100.0%; Score 1614; DB 2; Length 309; 100.0%; Pred. No. 1.1e-129; ive 0; Mismatches 0; Indels 0

Query Match 100. Best Local Similarity 100. Matches 309; Conservative

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TYPE: PRT
CRGANISM: Human
US-09-422-869-20

9 9 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH

MNCTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT

PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFFLLGF 180

120

240

YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR 240

181

121

241

Sequence

LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS 300

88 Sequence 88, Appl Sequence 22, Appl Sequence 373, App Sequence 16, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 166, App Sequence 166, App Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 31, Appli Se	TYPB 2 DIABETES
US-10-314-048A- US-09-979-603-2 US-09-745-842-1 US-09-777-173D- US-08-8148-708-2 US-08-8148-708-2 US-08-8148-708-2 US-08-813-948- US-08-98-876-9 US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-442-134A- US-08-443-134A- US-08-443-134A- US-08-443-134A- US-08-559-524A- US-08-559-524A- US-08-513-9748-	9 9 ATMENT OF 422,869 ,175
19.7 19.6 19.6 19.5 19.5 19.5 19.5 19.2 19.2 19.2 19.2 19.1 19.1 19.1 19.1	ALIGNMES SULT 1  -09-422-869-20 Sequence 20, Application US/09422869 Patent No. 6235481 GENERAL INFORMATION: APPLICANT: POLONSKY, KENNETH S. APPLICANT: POLONSKY, YUKIO APPLICANT: ODA, NAOHISA APPLICANT: COX, NANCY J. APPLICANT: SEERNAN, SEAMUS APPLICANT: STERNAN, SEAMUS APPLICANT: STERNAN, SEAMUS APPLICANT: STENICH I APPLICANT: APPLICATION WINSER: US/09/422,86 CURRENT PRILING DATE: 1999-10-21 EARLIER APPLICATION NUMBER: 60/134,175 EARLIER APPLICATION NUMBER: 00/134,175
28 317.5 29 317.5 31 315.5 32 315.5 34 316.5 35 310.5 36 310.5 37 310.5 36 308.5 40 308.5 41 308.5 42 308.5 44 308.5 44 308.5 44 308.5 44 308.5 44 308.5 44 308.5	MESULT 1  19.09-422-869-20  Sequence 20, Application 1  Separation 10. 6235481  GENERAL INFORMATION:  APPLICANT: POLONSKY, KEN  APPLICANT: ODA, NAOHISA  APPLICANT: COX, NANCY J.  APPLICANT: COX, NANCY J.  APPLICANT: SEERNAN, SEAM  APPLICANT: APPLICANT: APPLICANT: COX, NANCY J.  APPLICANT: APPLICANT: APPLICANT  APPLICANT: APPLICANT: COX, NANCY J.  APPLICANT: BELL, GRABEB  TITLE OF INVENTION: METHOR APPLICATION NUMB  CURRENT FILING DATE: 199  CURRENT FILING DATE: 199  KEALLIER FILING DATE: 199  NUMBER OF SEQ ID NOS: 307  SEQ ID NOS: 306  LEWATH: 306

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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
FILE REPERRENCE: 22.086.CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 KFGDIPCRIMLFMIAMNRQGSIIPLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLWG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 WSLRQR---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQNC 266
                         249 --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKSQDSLC 305
                                                     | : | | | : | | | : | | 281 TNCFLERFAKIMYPITLCLATLNCCFDPFIXYFTLESFQKSFYI-----NAHIRMESLF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 LVIGSLV--ARWLLGIQEGG--FCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKVV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 LGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRSDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LGVLLVLGLLLNSLALWVPCCRMQQWTETRIYMTNLAVADLCLLCTLPPVLHSLRDTSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 PL----COLSOGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPROAAAVCAVLWV
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Best Local Similarity 34.2%; Pred. No. 8.5e-25;
Matches 94; Conservative 48; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARR: PRECRILIN VERSION 3.1
                                                                                                                                                                                                                                                                                           Sequence 159, Application US/10314048A Patent No. 6902902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowitz, Kevin P.
Behan, Dominic P.
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Unett, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi, Bryan
Leonard, James
Hakak, Yaron
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dang, Huong T.
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                                                                                                                       306 VT 307
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                                                                                                                                                                                                    Sequence 2, Application US/08781250
Patent No. 6010877
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Bergema, Derk
APPLICANT: Bergema, Derk
APPLICANT: Mao, JOYCe Yue
TITLE OF INVENTION: CDNA CLONE HE8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSS:
ADDRESSE: SmithKline Beecham
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYWAKEFQEASALAVAPRAKAHKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AVYSUVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 CSLKVVTALAQRPPTDVGQAEAT-RKAARMVWANLLVFVVCFLPLHVGLTVRLAVGWNAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AYLGVILVIGILINSLALMVPCCRMQQWTBTRIYMTNLAVADLCLLCTLPP-VLHSLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 402; DB 2; Length 370;
34.1%; Pred. No. 1.6e-26;
tive 60; Mismatches 111; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PASTEM: DOS
SOFTWARE: PASTEM: DOS
SOFTWARE: PASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
FILING DATE: 10-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATG50043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT
NAME: William T. Han,
REGISTRATION NUMBER: 34,344
REFRENCE/DOCKET NUMBER: ATGS
TREECOMMUNICATION INPORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 370 anino acids TYPE: amino acid strandedness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 34.1
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U8-08-781-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                             301 QDSLCVTLA 309
                                                                                              ODSLCVTLA 309
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GENERAL INFORMATION: 셤 셤 ò 셤 a ò 셤 à ઠે ઠે APPLICANT: LOWIZ, Kevin P.
APPLICANT: LOWIZ, Kevin P.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: For the Treatment of Metabolic-Related Disorders
FILE REPERENCE: 22.036.CIP
CURRENT FILING DATE: 2002-12-06
FRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2001-11-27
PRIOR PELING DATE: 2001-11-27
PRIOR PELING DATE: 2002-07-29
PRIOR PELING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOUTHARE PERCENTION NUMBER: 60/410,747
PRIOR FILING DATE: 2002-09-13 94 KFGDIP-CRLMLFMLAMNRQSSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLM 152 ::| || ::| || ::| || ::| ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || : 82 DISDIPLOOLSQGIYLINRYMSISLVIAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141 142 VLVIGSLV--ARWLLGIQEGG--FCFR-STRHNP--NSMRFPLLGFYLPLAVVVFCSLKV 194 153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMF-LLEFFLPLGIILFCSARI 211 195 VTALAQRPPIDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----NA 247 ||: ||| |||||||||| || 34 LGLEFIFGILGNGLALMIFCFHLKSWKSSRIFLFNLAVADFLLIICLFFLMDNYVRRWDW 93 27 LGVLLVIGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSL-----R 81 23.3%; Score 375.5; DB 2; Length 363; 34.1%; Pred. No. 2.8e-24; 267 EVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301

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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 222, Application US/09170496D
Patent No. 6555339
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AERN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
CURRENT PILING DATE: 1998-10-13
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PL----CQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 NPGDIP-CRLVLFWFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 VLVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 VVTALAQRPPIDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----N 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSIROR---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLAHTSGTQ 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVL----HSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                    ; Score 368.5; DB 2;
; Pred. No. 1.2e-23;
48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                      22.8%;
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Best Local Similarity 34.3*
Matches 95; Conservative
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APPLICANT: Behan, Dominic P
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; ORGANISM: Homo sapiens
US-09-170-496D-222
                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
US-09-170-496D-108
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Best Local Similarity
Matches 94; Conserv
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Leonard, James
                 Hakak, Yaron
Liaw, Chen
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APPLICANT: Chen, Ruoping
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-048A-135
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Best Local Similarity
Matches 95; Conserv
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US-09-875-076-4
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                                                                                                                       153 GITVGLTVHLLKKKLL-IQNGPANVCISFSICHTFRWHBAMF-LLBFLLPLGIILFCSAR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 VVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----N 246
94 KFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNWTAAIISCLLWG 153
                               143 LVIG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKV 194
                                                               154 ITVGLTVHLLKKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLLPLGIILFCSARI 211
                                                                                                  195 VTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCFLPLHVGLTVRLAVGW-----NA 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 VLVIG---SLVARWILGIQEG--GFCFR-STRHNF--NSMRFFLLGFYLPLAVVVFCSLK 193
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                                                                                                                                                                                                                                                                               34 LGLEFIFGLIGNGLALMIFCPHLKSWKSSRIFLFNLAVADFLLIICLPFVMDYYVRRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVL-----HSLR
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                                                                                                                                                                   248 CALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
                                                                                                                                                                                          266 CEVYRSVDLAPPITLSFTYMNSMLDPVVYYFSSPSF 301
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Farent No. 6902902
GENERAL INPORMATION:
APPLICANT: Unest, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Connolly, Daniel
APPLICANT: Choi, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-10-314-048A-135
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US-09-944-807-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 21
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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APPLICANT: LIAW, CHEN
APPLICANT: LOWIZ, Kevin P.
APPLICANT: Lowiz, Kevin P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Michael
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION NUMBER: U0/995,511
PRIOR PELING DATE: 2002-03-12
FRIOR PILING DATE: 2002-03-12
FRIOR PILING DATE: 2002-07-29
FRIOR PILING DATE: 2002-07-29
FRIOR PILING DATE: 2002-09-13
FRIOR APPLICATION NUMBER: 60/410,747
FRIOR APPLICATION NUMBER: 60/4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 VVTALAQRPPTDVGQAEATRKAARMVMANLLVFVVCFLPLHVGLTVRLAVGW-----N 246
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APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOGO

CURRENT PELLIGATION NUMBER: US/09/875,076

CURRENT FILING DATE: 2001-06-06

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 60/120,416

PRIOR FILING DATE: 60/120,416

PRIOR PLING DATE: 60/120,416

PRIOR PLING DATE: 60/120,416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 368.5; DB 2;
; Pred. No. 1.2e-23;
48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09875076
Patent No. 6869776
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1 Similarity 34.3%;
95, Conservative 46
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-UN-1995
CLASSIFICATION 435
PRIOR APPLICATION NOMER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   : LI, YI
: CAO, LIANG
: NI, JIAN
: NI, JIAN
: GENTZ, REINER
: BULT, CAROL J.
: SUTTON III, GRANGER G.
: ROSEN, CRAIG A.
                                                               Sequence 8, Application US/08467948A, Patent No. 5998164, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           E: STERNE, KESSLER,
1100 NEW YORK AVE.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 344 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.2%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202-371-2540
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WASHINGTON
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APPLICANT:
APPLICANT:
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                                               US-08-467-948A-8
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 VWANLLVFVVCFLPLHVGLTV----RLAVGWNACALLETIRRALYITSKLSDANCCLDAI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AVADLCLLCTLP----FVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 RYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLV-----ARWLLGIQEGGFCFRS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STINSSVLPCPDYRPTHRIALVVY-SLVLAAGLPIANALALWVFLRALRVHSVVSVXMCNL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 NTCGSSDLTWP---PAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNL
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33.7%; Pred. No. 4e-23;
tive 47; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                   REILING DATE: 1999-05-28

REPLICATION NUMBER: 60/137,131

REILING DATE: 1999-05-28

RELING DATE: 1999-06-29

REPLICATION NUMBER: 60/11,448

REPLICATION NUMBER: 60/156,653

REPLICATION NUMBER: 60/156,633

REPLICATION NUMBER: 60/156,633

RELING DATE: 1999-09-29

RELING DATE: 1999-09-29

RELING DATE: 1999-09-29
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                                                                                           R FILING DATE: 1999-03-12

R APPLICATION NUMBER: 60/136,436

R FILING DATE: 1999-05-28

R PILING DATE: 1999-05-28

R FILING DATE: 1999-05-28

R RILING DATE: 1999-05-28

R FILING DATE: 1999-05-28
                   APPLICATION NUMBER: 60/123,946
FILING DATE: 1999-03-12
APPLICATION NUMBER: 60/123,949
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APPLICATION NUMBER: 60/157,294
FILING DATE: 1999-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-09-29
APPLICATION NUMBER: 60/157,280
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FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/156,634
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FILING DATE: 1999-10-01
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DATE: 1999-02-26
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Best Local Similarity 33.7%
Matches 109; Conservative
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125 RGLRSPRQAAAVCAVLWVLVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176 222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY 278 176 TWKTYLSRIVIFIEIVGFFIPLILAVICSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124 ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221 334 HLIFCFCFVPYNINLILYSLVRTQTFVNCSVVAAVRTMYPITLCIAVSNCCFDPIVYYF 293 6 SSHCFYNDSFKYTLYGCMFSMVFVLGLISNCVAIYIFICVLKVRNBTTTYMINLAMSDLL 10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC Gaps 43; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR2 Length 344; 22.4%; Score 361.5; DB 1; Length 29.2%; Pred. No. 4e-23; trive 68; Mismatches 107; Indels GOLDSTEIN & FOX P.L.L.C. NW, SUITE 600 MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIN RELEASE #1.0, VERSION #1.30 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600

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69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TWKTYLSRIVIFIEIVGFFIPLILNVTCSSMVLKTLTK--PVTLSRSKINKTKVLKMIFV 233
                                       222 NLLVFVVCFLPLHVGLTVRLAVGWNA---CALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.3%; Score 360.5; DB 1; 30.0%; Pred. No. 4.3e-23; tive 64; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                         GENTZ, REINER
BULT, CAROL J.
                                                                                                                                                                                                                                                              Sequence 30, Application US/08467948A Patent No. 5998164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 302 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 amino acids
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not relevant
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CAO, LIANG
NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                       279 MAKEFQEA 286
                                                                                                                                                  : | :
294 TSDTIQNS 301
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Matches 90; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: siz
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                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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                                                                                                                                                                                                            APPLICANT: LIY YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: NI, JIAN
APPLICANT: NI, JIAN
APPLICANT: BULT, REBUT
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: POLYMUCLECTICES BROOGING HUMAN G-Protein
TITLE OF INVENTION: COULLED RECEPTOR GPRI
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.4%; Score 361.5; DB 2; Length 344; 29.2%; Pred. No. 4e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INPORMATION:
NAME: STEEFE, RRIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEFFE, BRICK K.
REGISTRATION NUMBER: 36,688
REPERBNCH/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMINICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Mismatches 107;
                                                                                                                                                                                                    MAIL.
LI, YI
: CAO, LIANG
f: NI, JIAN
TT: GENTZ, REINER
TTI, CAROL J.
TII, GRANGER G.
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                                                                                                                                                          ; Sequence 8, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 344 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                279 MAKEFQEA 286
                                                        294 TSDTIONS 301
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Best Local Similarity
Matches 90; Conserva
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                                                                                                                     RESULT 11
US-08-467-947A-8
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
TITLE OF INVENTION: 22.036.CIP
CURRENT TILING DATE: 20.02-12-06
CURRENT FILING DATE: 2002-12-06
PRIOR PILING DATE: 2002-03-12
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR FILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 TALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-----NAC 248
                                                                                                                                                                                                            222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                                                                     ------LLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARWWA 221
61 FVFTLPFRIYYF-VVRNWPPGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 119
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                                                       RGLRSPROAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 137, Application US/10314048A; Patent No. 6902902
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Connolly, Daniel
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Behan, Dominic P
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Hakak, Yaron
Liaw, Chen
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Choi, Bryan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-314-048A-137
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APPLICANT:
APPLICANT:
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         RGLRSPRQAAAVCAVLWVLVI-GSLVARWLLGIQEGGFCFRST-RHNFNSMR-----FP- 176
                                                 222 NLLVFVVCFLPLHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICYYY 278
                                                                                                                                                                                                                                                                                   9
                                                                                                                              -----LIGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWA 221
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APPLICANT: CAO, LIANG
APPLICANT: CAO, LIANG
APPLICANT: N. JIAN
APPLICANT: GENTZ, REINER
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: POLYMUCLECTICES BROOGING Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADD
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COMPUTER: TEMPOPY DISK
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PATENTIN RELEASE #1.0, VERSION #1.30
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN 1995
CLASSIFICATION 1435
PRIGNE APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR.1995
ATTORNEY/AGENT INPORMATION:
NAME: STEPPE, ERIC K.
NAME: STEPPE, ERIC K.
REGISTRATION NUMBER: 36,688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1488.1140002/EKS/KLM
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-467-947A-30
is Sequence 30, Application US/08467947A
is Detent No. 6090575
igeneral Information:
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SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET UNMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
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Best Local Similarity 30.0%
Matches 90, Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
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APPLICANT: Letrer, Michael TILE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof FILE OF INVENTION: for the Treatment of Metabolic-Related Disorders FILE REFERENCE: 22.U56.CIP CURRENT APPLICATION NUMBER: U5/10/314,048A CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -VLHSLRD----TSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ROAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFR-----STRHNFNSMRFPLLG 179
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33.2%; Pred. No. 2.1e-21;
tive 48; Mismatches 114; Indels 53; Gaps
                                                                                                                                                                                        : :: | : | : | | | 264 DIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSF 298
                                                                                                                                249 ALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283
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PRIOR FILING DATE: 2002-03-12
PRIOR PELING DATE: 2002-03-12
PRIOR PELING DATE: 2001-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 161
SOFTWARR: PALENTIN Version 3.1
SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 157, Application US/10314048A; Patent No. 6902902; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unett, David J.
Chen, Ruoping
Richman, Jeremy
Connolly, Daniel
Dang, Huong T.
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Behan, Dominic P.
Chalmers, Derek T
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Best Local Similarity 33.24
Matches 107; Conservative
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Hakak, Yaron
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi, Bryan
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US-10-314-048A-157
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ORGANISM: Rat
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Search completed: February 9, 2006, 01:02:27 Job time : 34.5 secs

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CS122237 Sequence
AK489206 Sequence
AK707957 Homo sapi
AK172786 Homo sapi
AC111190 Homo sapi
AC111190 Homo sapi
AY893518 Synthetic
AR153299 Sequence
AK693519 Sequence
AK671157 Sequence
AK671157 Sequence
AK6898987 Homo sapi
AK152389 Sequence
AK68988452 Sequence
AK18748 Homo sapi
AK11540 Homo sapi
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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AF027957
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<u> </u>	REFERENCE AUTHORS TITLE JOURNAL FEATURES . SOUK	o O	Hominidae; H 1 Golz, S. Biagnostics Diagnostics Parcein-coup Parcein. WO ou Bayer Health Loc 1. 1. //or //or	Hominidae; Homo.  Golz, S.  Golz, S.  Jamostics and therapeuti protein-coupled receptor 3  Patent: WO 205059546-A 1  Bayer HealthCare AG (DE)  Location/Qualifie  1. 930  /organism="Homo E/mol_type="unassi"/Ab_xref="taxon:	her ece 954 AG 1/Qu """"	; Homo.  cs and therapeutics for disease oupled receptor 35 (gpr35) 0 2005059546-A 1 30-JUN-2005; lthCare AG (DE) 1. 930 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	eases 5 ;	associated	with	ຽງ
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    /organism="Homo sapiens"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 491 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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us-10-083-168-84.rge

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Homo sapiens CDNA FLJ23947 fis, clone HEP05863, highly similar to G protein coupled receptor GPR35.

AK172786
AK172786.

AK172786.1 GI:4707780
oligo capping; fis (full insert sequence).

Homo sapiens (human)
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Sugano, S. and Suzuki, Y.
Direct Submission

Submitted (122-APR-2004) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:flodna@mail.ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Pax:81-3-5449-5416)
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Ota,T.,
Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
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                                                                       AF027957 1299 bp DNA linear PRI 17-FEB-1998
Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds.
AF027957
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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O'Dowd, B.F.
Direct Submission
Submitted (03-OCT-1997) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd., Toronto, ON MSS 1A8, Canada Location/Qualifiers
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1 (bases 1 to 1299)

O'Dowd, B.F., Nguyen, T., Marchese, A., Cheng, R., Lynch, K.R., Heng, H.H., Kolakowski, L.F. Jr. and George, S.R.
Discovery of three novel G-protein-coupled receptor genes Genemics 47 (2), 310-313 (1998)
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/mol_type="genomic DNA"
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/map="2q37.3"
/gene="GPR35"
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HTG; HTGS PHASE; HTGS DRAFT; HTGS FULLTOP HOMO Sapiens (human)
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1 (bases 1 to 169391)
Waterston, R.H.
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Waterston, R.H.
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology, cDNA library construction, 5. & 3. - end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
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Pred. No. 2.4e-120;
0; Mismatches 5;
                                                                                                                                                                                                                               |cell_type="hepatoma"
|clone_lib="HEP"
|note="cloning vector pME18SFL3"
                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP05863"
                                                                                                                                                                                                                /cell_line="HepG2"
                                                                                                                                                                                                                                                                                                                         99.14;
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ACI11190 169391 bp DNA linear HTG 20-JUN-2002 Homo sapiens chromosome 2 clone RP13-511H14, WORKING DRAFT SEQUENCE, 7 unordered pieces.
1723 ACCAGCAAGCTCTCAGATGCCAACTGCTGGCTGGACGCCATCTGCTACTACTACATGGCC 1782
                                                                                                                                           1783 AAGAAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (18-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (Dases 1 to 169391)
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Submitted (20-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                            900
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                        841 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC
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On Jun 14, 2002 this sequence version replaced gi:18699976.
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Chemistry: Dye-primer BT; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167477 bases at least Q40
Consensus quality: 168108 bases at least Q20
Consensus quality: 168194 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 186791; sum-of-contigs
Quality coverage: 9.60 in Q20 bases; sum-of-contigs
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Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Contact: Project Information
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FEATURES

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

E 1 (bases 1 to 930)
S Marren, C.N., Aronstam, R.S. and Sharma, S.V.
I Unpublished
E 2 (bases 1 to 930)
S Marren, C.N., Aronstam, R.S. and Sharma, S.V.
S Warren, C.N., Aronstam, R.S. and Sharma, S.V.
I Unpublished
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Homo sapiens G-protein coupled receptor 35 (GPR35) gene, complete
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Homo sapiens
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                   it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

99.1%; Score 922; DB 14; Length 169391;
Best Local Similarity 99.5%; Pred. No. 8.8e-121;
Matches 925; Conservative 0; Mismatches 5; Indels 0;
                                                  5580: contig of 5580 bp in length
5581 5580: gap of unknown length
5681 17193: contig of 11513 bp in length
17293: gap of unknown length
17294 39574: contig of 22281 bp in length
17295 gap of unknown length
17295 64394: contig of 24720 bp in length
17295 82827: contig of 18333 bp in length
1729 82827: contig of 18333 bp in length
1729 119152: contig of 18225 bp in length
1723 119252: gap of unknown length
1723 169391: contig of 50139 bp in length
1723 169391: contig of 50139 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /estimated_length=unknown
119253. .169391
/note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /estimated length=unknown
64495. .82827
/note="assembly_name:Contig24"
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82928. .119152
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119153. .119252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39675. .64394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5681. .171<u>9</u>3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          estimated length-unknown
7294. .39574
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vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             estimated_length=unknown
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="2"
/clone="RP13-511H14"
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ORIGIN

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This clone is available from RZDD;
Contact RZPD (customer.serviceerzpd.de) for further information.
Contact RZPD (customer.serviceerzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLHIJ1000.01X
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTTTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM_005301 (GI:33695096) we found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR541765 930 bp mRNA linear PRI 29-JUN-2004 Homo sapiens full open reading frame cDNA clone RZPDo834D0330D for gene GPR35, G protein-coupled receptor 35; complete cds, incl.
                                                                                                                                                                                                                                                                                 900
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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834D0330D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                           840
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Alalleck, A., Eberri, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Bliect Submission
Submitted (28-JUM-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Peld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 930)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Pax: +49 30 32639 111
                                                    721 CTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCGTCGCGCCCCTGTACATA
                                                                                                                                                                                                                                                            781 ACCAGCAAGCTCTCAGATGCCAACTGCTGGCCTGGACGCCATCTGCTACTACTACTACATGGCC
                                                                                                                                                                                                                               AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCCACAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pull ORF shuttle clone, Gateway (TM), complete cds. Homo sapiens (human)
Homo sapiens
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VERSION
KEYWORDS
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PCCRWQQWTERRIYWRLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYM
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VWANLLVFVVCPLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICY
YYMAKEFQEASALAVAPSAKAHKSQDSLCVTLA"
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                                                                                                                                                                                                                                                                       product="G-protein coupled receptor 35" 
protein id="AAP32299.1" 
/db_xref="GI:30526188"
                                                                                                                                                                             'product="G-protein coupled receptor 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 920.4; DB 8;
Pred. No. 4.9e-120;
0; Mismatches 6;
sapiens"
                     Ltype="genomic_DNA"
_xref="taxon:9606"
organism="Homo
                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                   /gene="GPR35"
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Best Local Similarity 99.4%;
Matches 924; Conservative (
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/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930 bp mRNA linear SYN 16-MAR-2005 sapiens clone FLH131000.01X G
35 (GPR35) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gareway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other sequences; artificial sequences.

1 (bases 1 to 930)

Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.
Cloning of human full-length CDS FLEXGene in
Gateway(TM) recombinational vector system
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                                               CTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCGCGCCCTCTAAAA
501 AGGCCACCCACCGACGTGGGGCAGGCAGGCCACCCCCCAAGGCTGCCCGCATGGTCTGG
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/transl_table=11
/product="G protein-coupled receptor 35"
/protein_id="AAX36555.1"
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/db_xref="taxon:32630"
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/gene="GPR35"
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  AA exchange(s) at position (first base of changed triplet): 880(ser->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAG46564.1"
/db_xref="G1:49456487"
                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDo834D0330D"
                                                                                                                                                                                                                                                             /lab host="DH5Alpha"
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Horlkawa, Y., Oda, N., Hanis, C.L., Bel
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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CCGCTGCGTGCCCGCGGGCTGCCCCCAGGCAGGCTGCGGCCGTGTGCGCGGTCTCTC
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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Mammila, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Pharmaceuticals AG (DE)
Location/Qualifiers
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1476 CAGGACTCTCTGTGCGTGACCCTCGCCTAA 1505
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhin; Hominidae; Homo.

El (Dases 1 to 1875)

Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del Bosque-Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S., Polonsky,K.S., Wel,S., Concannon,P., Iwasaki,M., Schulze,J., Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and Bell,G.I.

Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus

In Nat. Genet. 26 (2), 163-175 (2000)

Direct Submission Submitted (02-SEP-1998) Howard Hughes Medical Institute, The University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL 60637, USA

2 (bases 1 to 1875) Horikawa, Y. and Bell, G.I.

1. 1875 /organiem="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="2"

Location/Qualifiers

/map="2q37" 576. .1505 /note="similar to GPR35"

CDS

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REFERENCE
AUTHORS
TITLE
JOURNAL
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/codon_start=1 /product="%0 protein-coupled receptor" /protein_id="AAG77965.1" /db_xref="GI:10503933"

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PCFRSTRHPFNSMAFPLLGFYLPLAVVVFCSLKVYTALAQRPPTDVGQARATRKAARM
VWANILVFVVCFLPHIYGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAICY
YYMAKEPQBASALAVAPSAKAHKSQDSLCVTLA"
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                                                                                                                                                                         Length 1875;
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Pred. No. 4.2e-120;
0; Mismatches 6;
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al Similarity 99.4%;
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arusyos7 Homo sapiens G protein-coupled receptor mRNA, complete cds. AF089087

AF089087.1 GI:10503932 Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS RESULT 12 AF089087

Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 65674)

1 horkawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M., Hiokio,Y., Lindner,T.H., Mashima,H., Schwarz,P., del Bosque Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S., Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulze,J., Baler,L.J., Bogardus,C., Groop,L., Boerwinkle,B., Hanis,C.L. and
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Genetic variation in the gene encoding calpain-10 is associated
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Homo sapiens map 2q37.3, genomic sequence.
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99.0%; Score 920.4; DB 6; Length 49136;
Best Local Similarity 99.4%; Pred. No. 2e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0;
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Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I. and Cox,N.J.
Polynucleotides encoding calpain 10
Patent: US 6235481-A 1 22-MAY-2001;
Location/Qualifiers
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Sequence 1 from patent US 6235481.
AR153289
AR153289.1 GI:15120821
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3 (bases I to 160111)
Waterston, R. H.
Direct Submission
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Submitted (08-SEP-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 160111)

Haakenson, W., Trani, L. and Schatzkamer, K.

The sequence of Homo sapiens BAC clone RP11-27M15

Unpublished (2001)

2 (bases 1 to 160111)

Waterston, R.H.
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Homo sapiens BAC clone RP11-27M15 from
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4 (bases 1 to 160111)
Waterston, R.H.
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Waterston, R.
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Direct Submission
Submitted (15-OCT-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Wilson, R.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
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This gene was based on gi(4885320)"
                                                                                                                                                                             Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catamses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACCe1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insert of the clone. This clone is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and respeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                              Submitted (15-ARR-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 8, 2002 this sequence version replaced gi:22091410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of AC080022 has been incorporated into AC124862 Location/Qualifiers
                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                         NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire inse
overlapped by AC011298 and AC110619.
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                                                                                                                                                                                                                                                           Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="GPR35"
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TFI ISSILESDBELVIDVIHEVAHSPRGNAVTNATWERMILSEGLATYAGRITTETY
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YYMAKEFQBASALAVAPSAKAHKSQDSLCVTLA
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//orce="Mono sapiens arginyl aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1), mRNB.; H NH002/M15.2
This gene was based on g1(20070295)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSDTEFHPIĞFHIPQVPEĞGRSQDAPPLLLQEPLLSCVPHRYAQEVSRLCLLPAĞTYK
VVPSTYLPDTEGAFTVTIATRIDRPSIHSQEMLGQFLQEVSIMAVMKT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(36727, .36756,37010, .37055,37320, .37519, 38465, .38726,38886, .39088,40103, .40383,40698, .40864,41360, .41501,43257, .43474,44396, .44592,45933, .46064,48355, .48495)
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38465. .38726,38886. .39088,40103. .40383,40698. .40864,
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// force="Homo sapiens calpain 10 (CAPN10), transcript variant 1, mRNA; H NH0027M15.3
This gene was based on gi(13186301)"
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11914. 12354
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44479. .44861
                                                                                                                                                                                                                                                                                                  11914. 12354
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Complement(36303. 48672)
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47989. .49<u>2</u>01
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                                                                                                                                                                                            5454 AIGAAIGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGGGATGAAG
                                                                                                                                                                                                                        5394 CTGGGCTTCTACGCCTACTTGGGCGTCCTGCTGGTGCTTAGGCCTGCTCAACAGCCTG
                                                                                                                                                                                                                                                           GCGCTCTGGGTGTTCTGCTGCCGCATGCAGTGGACGGAGACCCGCATCTACATGACC
                                                                                                                                                                                                                                                                    5334 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGCGAACGGAACGGACCCGCATCTACATGACC
                                                                                                                                                                                                                                                                                               AACCTGGCGGTGGCCGACCTCTGCCTGCTGTGCACCTTGCCCTTCGTGCTGCTCCTG
                                                                                                                                                                                                                                                                                                                                 5214 CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGCATCTACCTGACCAACAGG
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    Gaps
                                                                                                                                                Query Match
99.0%; Score 920.4; DB 8; Length 160111;
Best Local Similarity 99.4%; Pred. No. 1.5e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0;
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 840

 bb
 4674
 ACCAGCAAGCTCTCAGATGCCAACTGCTGGACGCCATCTGCTACTACTACTGCCT
 4615

 bb
 4614
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Search completed: February 11, 2006, 04:54:32 Job time : 5119 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- nucleic search, using sw model OM nucleic February 11, 2006, 00:25:50 Run on:

; Search time 684 Seconds (without alignments) 9061.643 Million cell updates/sec

US-10-083-168-84 930 Title: Perfect score:

1 atgaatggcacctacaacac.....tgtgcgtgaccctcgcctaa 930 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 seqs, 3332346308 residues Searched: 9993994 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum Maximu Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_21:* Database

genesequ1990s:* genesequ2000s:* genesequ2001as:* genesequ2001as:* genesequ2002as:* genesequ2003as:* genesequ2003as:* geneseqn2003ds:* geneseqn2003cs:* geneseqn2004as:* geneseqn2004bs:* geneseqn2005s:* geneseqn1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Abs73401 DNA encod	Abs73345 cDNA enco	Abz42852 Human G p	Adb67672 Human G p	Ado29916 Human GPC	Adv73165 Human col	Aeb15038 cDNA enco	Aaz50891 Human rec	Aaa27485 Human G p	Ada84068 Human GPR	Ado78086 Human GPR	Aaa27475 NIDDM1 re	Adf70563 Orphan re	Adr10415 Full leng	Aaz35390 Human G-p	Abz35525 Human gen			Adul1275 Solid tum
SUMMARIES	ΩI	ABS73401	ABS73345	ABZ42852	ADB67672	2 ADO29916	4 ADV73165	4 AEB15038	AAZ50891	AAA27485	ADA84068	2 ADO78086	AAA27475	0 ADF70563	3 ADR10415	AAZ35390	ABZ35525	2 ADP28534	2 ADO30206	3 ADU11275
	å Query Match Length DB	930 6	930 6	930 8	930 9	930 1	930 1	930 1	1369 3	1875 3	1875 8	1875 1	49136 3	1644 1	3811 1	1043 3	1989 6	858 1	924 1	599 1
	& Query Match	100.0	99.5	99.5	99.5	99.5	99.5	99.5	99.1	99.0	0.66	99.0	99.0	98.8	98.6	98.5	96.8	90.1	59.1	55.3
	Score	930	925.2	925.2	925.2	925.2	925.2	925.2	922	920.4	920.4	920.4	920.4	919	917.2	915.6	900	838	549.2	514.2
	Result No.	-	8	m	4	S	9	7	60	ō	10	11	12	13	14	15	16	17	18	19

Acl58361 Human col	Aad10133 Mouse G p	Abl35067 Murine cD	Adf87215 Single nu	Aaa30740 DNA encod	Adc22744 Human G p		Aaa30581 Human G p		Acc78113 Human G p	Adc22522 Human G p	Adh13995 Human GPR	Ado29766 Human nov	Abz34905 Human gen	Ade84894 Farnesyl	Aca56831 Human sig	Adi56627 Human pol	Aad50858 Human G-p	Abz42741 Human G p	Human		Ads75991 Human GPR	Aad26831 Human G-p	Adl71938 Human GPR	Human	Adu06778 Human GPR
1 ACL58361	AAD10133	ABL35067	) ADF87215	AAA30740	D ADC22744	D ADH14217	AAA30581	AAD26832	ACC78113	D ADC22522	0 ADH13995	2 ADO29766	ABZ34905	0 ADE84894	0 ACA56831	2 ADI56627	AAD50858	ABZ42741	2 ADF17570	2 ADO28684	3 ADS75991	AAD26831	2 ADL71938	3 ADS19844	3 ADU06778
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## ALIGNMENTS

Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; mutant; ds. DNA encoding human GPCR GPR35 mutant A216K. ABS73401 standard; DNA; 930 BP (first entry) WO200268600-A2. Homo sapiens. Synthetic. 04-DEC-2002 ABS73401; RESULT 1 ABS73401 

06-SEP-2002.

26-FEB-2002; 2002WO-US005625.

26-FEB-2001; 2001US-0271913P.

(AREN-) ARENA PHARM INC.

Leonard JN; Maciejewski-Lenior D, Behan DP, Chalmers DT, Liaw CW, Char...

WPI; 2002-706980/76. P-PSDB; ABG95172.

New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.

Example 2; Page 188-189; 201pp; English.

The present invention relates to transmembrane receptors, particularly

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cDNA encoding human GPCR GPR35
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                                                                                                                                                ABS73345 standard; cDNA; 930
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Best Local Similarity 99.7%;
Matches 927; Conservative
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P-PSDB; ABG95159.
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endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension reflux disease, depression, migraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhintis, and angina. The present
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The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCR8), mutant (nonendogenous) versions of the GPCR8, and the polynucleotide sequences encoding them. The GPCR8 are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, magraine, schizophrenia, ulcers, psychotic disorders, asthma, bronchospaem, anaesthesia, myocardial infarction (MI), anxiety, prostatic hypertaplasia, epilepsy, prostate cencer, sequence encodes an endogenous human GPCR.
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                                  841 AAGGAGTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 900
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inverse agonist compounds for treating diseases associated with GPCR.
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Pred. No. 1.9e-175;
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                                     AACCTGGCGGTGGCCGACCTCTGCCTGTGCACCTTGCCCTTCGTGCTGCACTCCCTG
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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease;
                                                                                                                                     Human G protein-coupled receptor GPR35 nucleotide SEQ ID NO:491.
                                  踞
                                  ABZ42852 standard; DNA; 930
                                                                                                       (first entry)
                                                                                                       04-MAR-2003
RESULT 3
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or osteoporosis, cardiomyopathy, inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia, memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nauses; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; ds Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; Disclosure; Fig 1; 523pp; English. (LIFE-) LIFESPAN BIOSCIENCES INC. 19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107. Roush CL, WPI; 2003-046718/04. P-PSDB; ABP82002. autoimmune diseases WO200261087-A2. Homo sapiens. 08-AUG-2002 Burmer GC, 

The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular GC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (1) an isolated antibody having high specificity and high affinity or aridity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are useful in the production of specific antibods. The peptides and antibodies are useful for diagnosing and designing drugs for gPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, immunological-related disease, catherosclerosis, bacterial, fungal, protozoa or viral infections, crecoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host cinflammation, allergies, Crohn's disease, diabetes, graft versus host cancer, allerge, parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory consistent, relations renal disorders, rheumachoid arthritis, trauma, ulcers, or hypotension, renal disorders, rheumachoid arthritis, trauma, ulcers, or used in munoassays and immunoadiagnosis, ABZ42231 to ABZ42869 encode proteins given in ABP81675 to ABP82018, which are used in

Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

exemplification of the present invention

GPCR

Gaps ô Length 930; Indels Score 925.2; DB 8; Pred. No. 1.9e-175; 0; Mismatches 3; 99.5%; 927; Conservative Similarity Query Match Local Best Loca Matches

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The present invention relates to a method for predicting pathological conditions in heart failure using expression of one of 17 gene sequences (ADB67763-ADB67678); or protein sequences encoded by the genes (ADB67648-ADB67662). The proteins and genes are useful for diagnosis, treatment and prevention of heart failure.
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99.7%; Pred. No. 1.9e-175;
cive 0; Mismatches 3;
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                                    27-FEB-2003; 2003WO-JP002228.
                                                                   28-FBB-2002; 2002JP-00054388.
15-APR-2002; 2002JP-00112228.
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Koishi R, Nakamaru K;
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GCCAACCTCCTGGTGTTCGTGGTCTTGCTTGCTGCCCTGCACGTGGGGGTGACAGTGCGC
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Zeng H;
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Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GPCR GPR35 polynucleotide, SEQ ID NO:1018.
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Mcilwain KL, Pav
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P-PSDB; ADO29394.
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The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR pen of the invention; a mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR polynucleotides of the invention. The invention intributed siscloses variants of the GPCR polyspetides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may comprise to the diagnosis, treatment or prevention of a wide variety of disorders of the adrenal gland; disorders (e.g., Alzhamer's disease, disorders of the adrenal gland; disorders (e.g., Alzhamer's disease, cancention; the adrenal gland; disorders of the colon or intestine syndrome); cardiocascular disorders (e.g., angina, cardiac arrhythmia or syndrome); cardiocascular disorders (e.g., angina, cardiac arrhythmia or syndrome); pleukemial); immune disorders (e.g., augina, cardiac arrhythmia or ALDS); bone and joint disorders (e.g., angina, cardiac arrhythmia or costeoprorsis); metabolic or nutritive disorders or the law or osteoporosis); metabolic or vitening, prostate, testis, skin, stomach, pancreas, spleen, thymwas and thyroid (e.g., cancers). The present sequence appeared or the present sequence appear did not form part of the printed specification; respectively form the abona were obtained in electronic formed the sequence argument disorders (e.g., cancers). The present disorders (e.g., ca
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99.5%; Score 925.2; DB 12; Length
Best Local Similarity 99.7%; Pred. No. 1.9e-175;
Matches 927; Conservative 0; Mismatches 3; Indels
               claim 151; SEQ ID NO 1018; 542pp; English.
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cadherin or its fragment. The antibody is useful in preparing a
composition for treating or preventing a cancer-associated disorder. The
present sequence represents a gene upregulated in human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                           AGGCCACCCACCGACGTGGGGGGGGGGCGCCGCGCAGGCTGCCCGCATGGTCTGG
                                                                                                                                             CTCGCAGTGGGGCTGGAACGCCTGTGGCCCTCTGGAGACGATCCGTCGCGCCCTGTACATA
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        TTCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC
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                                                                                                                                                                                                                                                                                                                                                                    ds; gene; cancer; neoplasm; cytostatic.
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A, Staten NR;
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Mazzarella RA,
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Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;
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                                                        al Similarity 99.7
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The invention relates to the use of human G-protein coupled receptor 35 (GPR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, interactly diseases, metabolic diseases, hematological disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The cherapeutic agents are screened by contacting a test compound with GPR35 cplypeptide, and detecting the binding of the test compound with GPR35 cplypeptide, and detecting the binding of the test compound to the specified diseases in a mammal, comprising determining the amount of the GPR35 polymucleotide in healthy and/or diseased mammals (CR spass) polymeleotide in a sample taken from the mammal, and determining the amount of the GPR35 polymucleotide in healthy and/or diseased mammals (CR seases in the mammal, comprising of the above specified diseases in the preparation of the pharmaceutical composition or for the regulation of GPR35 activity of the pharmaceutical composition or for the regulation of GPR35 activity or preparation of the pharmaceutical composition, comprising identifying the comparation of the pharmaceutical carrier. GPR35 regulator, determining whether the regulator ameliorates the cymptoms of the above specified diseases in a mammal, and combining the creening therapeutic agents for treating cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, concerning therapeutic agents for treating cardiovascular disorders and urological disorders repiratory diseases, cancer disorders and mammal, e.g. humans (preferably), dogs, cats, cows, horses, rabbits, and mammal, e.g. humans cequally and the page of the page of the page of the page of the
                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR; screening; cardiovascular disease; gastrointestinal disease; liver disease; cancer; neoplasm; metabolic disorder; nemeatological disease; respiratory inflammation; neurological disease; urological disease; urological disease; ardiovascular-gentinal gen.; hepatotropic; cytostatic; metabolic; antianemic; respiratory-gen.; antiinflammatory; neuroprotective; uropathic; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUN01 cDNA library. This sequence is expressed in heamelapoletic/immune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiarthritic, antidabetic, dereopathic, antiallergic, antianemic, antiatethmatic, antidabetic, dereopathic, antiallergic, antianemic and prevention of disorders associated with HRAP expression, especially eacil proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AlDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable
                                                                                                                                                                                                                                                                   cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic; antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological; neuroprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; call proliferative; autoimmune; inflammatory; allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.
                                                                                                                                                                                             Human receptor-associated protein cDNA from Incyte clone 3083742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guegler KJ;
                                                                                                                                                                                                                                               receptor-associated protein; HRAP; Incyte clone 3083742;
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99.1%; Score 922; DB 3; Length 1369;
Best Local Similarity 99.5%; Pred. No. 8.8e-175;
Matches 925; Conservative 0; Mismatches 5; Indels
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                           AAZ50891 standard; cDNA; 1369 BP
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/product= "HRAP"
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Corley NC, Baughn MR;
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P-PSDB; AAY69989.
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CC almed methods for screening for a propensity for type 2 diabetes conclude are based on detection of a polymorphism in a calpain encoding concluder are hand are also claimed for identifying modulators of calpain activity, and using these modulators to treat diabetes, in companion mediated glucose transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oda N, Sreenan S, Zhou Y, Otani K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;
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                                                                                                                                                         (pos:1095. .1097, aa:Arg) (pos:1455. .1457, aa:Arg)
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Pred. No. 1.9e-174;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY79576, AAY79574, AAY79576
                                                                                                 Location/Qualifiers
576. .1505
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Bell GI, Cox NJ;
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(TEXA ) UNIV OF TEXAS SYSTEM.
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Best Local Similarity 99.4%;
Matches 924; Conservative
                                                                                                                                                                                                                                                                                                                                                                    99US-0134175P
                     diagnosis; therapy; ss.
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                                                                                                                                                                                                                             WO200023603-A2.
                                                                                                                                                                                                                                                                                                         21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                 21-OCT-1998;
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polonsky KS,
Hanis CL, B
                                                                                                                                                                                                                                                                   27-APR-2000
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1116 TACCHGCCCTGGCCGTGGTCTTCTGCTCCTCGAAGTGGTGACTGCCCTGGCCCAG 1175
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936 CCGCTGCGTGCCCGCGGGCTGCGGTCCCCCAGGCAGGCTGCGGCCGTGTGTGCGCGGTCCTC 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing inhibitor of expression or activity of specific tumor-associated antigens, useful for treating cancers, also related
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                                                                                                                                                                      TICTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCTGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparation of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTS expressed in normal tissue in order to identify ESTS that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced of the invention is also useful for determining the progression of colon cancer in a human, for detecting tumour cell, and for regulating or preventing the growth of a tumour cell, and for regulating or useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypebide of the invention is useful as an animal. The present sequence encodes a continuous cell and the present encodes a continuous cell and the propersed of the invention is the continuous cell and the present encoded by the invention of the continuous cell and the propersed of the invention is the continuous cell and the propersed of the invention is the continuous cell and the propersed of the invention is the continuous cell and the propersed of peptides encoded by the invention of the invention of the continuous cell and the continuous cell
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                                                                                                                                                                                                                                                                                                                                                                                         Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.
                                                                                                                                                                                                                                                          Kozlov AP, Lobashev AV, Krukovskaya LL;
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Pred. No. 1.9e-174;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogen for vaccinating an animal. The pr
tumour-associated antigen of the invention.
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                                                                        30-MAY-2001; 2001US-0293999P.
22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
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Best Local Similarity 99.4%;
Matches 924; Conservative (
                        30-MAY-2002, 2002WO-IB004189
                                                                                                                                                                                                                                                       Baranova AV, Yankovsky NK,
                                                                                                                                                                                              (BIOM-) BIOMEDICAL CENT
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P-PSDB; ADA84069.
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                                 The invention relates to pharmaceutical compositions that comprise an agent that inhibits the expression or activity of a tumour-associated antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical compositions and related compositions, are used for treatment of diseases associated with (abnormal) expression of TAG, specifically cancer e.g. of lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney or cervix, also melanoma. Compositions containing TAG, or related nucleic acid, antibodies or host calls, are also useful for diagnosis and monitoring of tumours. The present sequence represents the human GPR35
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                                                                                                                                                     Length 1875;
                                                                                                                                  Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;
                                                                                                                                                                      Indels
                                                                                                                                                    Score 920.4; DB 12;
Pred. No. 1.9e-174;
0; Mismatches 6; 1
 compositions for diagnosis and monitoring
                   ID NO 1; 124pp; German.
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Best Local Similarity 99.4%; Pri
Matches 924; Conservative 0;
                   Claim 1; SEQ
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                                                                               AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGCTCCCCGTGCTAAGGC
ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGGACGCCATCTGCTACTACTACTACATGGCC
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/note= "G-allele has a frequency of 0.94
(Japanese)"
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                                                                                                                                              CAGGACTCTCTGTGCGTGACCCTCGCCTAA 1505
                                                                                                                              CAGGACTCTCTGTGCGTGACCCTCGCCTAA 930
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/note= "G-allele has a frec
whites of German ancestry"
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/*tag= h
/number= 3*
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/*tag= c
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5283. .5468
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5283. .5479
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'number= 1
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9010. 9175
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/number = 6
/note = "TGA, 9013. 9015"
9176. 9490
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9491. 9771
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/rtag= ad
/number= 14
30981..31445
/rtag= ae
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31446..32175
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12864. .13116
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13117. .13569
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8373. .8514
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The present sequence is that of a 49,136 bp region located within the NIDDM1 region of human chromosome 2. It includes the CAPN10 gene that encodes a novel calpain-like cysteine protease, designated calpain 10, and a gene encoding a G protein coupled receptor, GPR35. Alternative splicing of calpain 10 mRNA generates a family of proteins. Isoforms 10a-16 (see ANY3957-74) are respectively encoded by exons 1-7,9-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11-13, 1-7,9-11,9-11-13, 1-7,9-11,9-11-13, 1-7,9-11,9-11-13, 1-7,9-11,9-11-13, 1-7,9-11,9-11-13, 1-7,9-11,9-11-13, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG
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P-BSDB; AAY79567, AAY79568, AAY79569, AAY79570, AAY79571, AAY79572,
AAY79573, AAY79574, AAY79576.
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Bell GI, Cox NJ;
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                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPP or OFF SHIANGED GFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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22-FEB-2002; 2002JP-00045728.
23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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                              GCCAACCTCCTGGTGTTCGTCTGCTTCCTGCCCCTGCACGTGGGGCTGACAGTGCGC
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AGGCCACCCACCGACGTGGGGCAGGCAGAGGCCACCCGCAAGGCTAAACGCATGGTCTGG
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Nagai K, Irie R;
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molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polymucleotide is a full length human cDNA sequence of the invention. NOTS: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the Buropean Patent Office, Vienna Sub-office.
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Pred. No. 9e-174;
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AAV58645), a novel member of the purinergic family of polypeptides and a
CP-protein coupled receptor. The invention provides GPR35A polymcleotides
CC having at least 70% identity with the present sequence, GPR35A
CC polypeptides, recombinant materials, and methods for their production.
CG GRR35A polypeptides can be used for identifying agonists and
antagonists/inhibitors, and for detecting diseases associated with
CC inappropriate GPR35A activity or levels. GPR35A polypeptides and
CC inappropriate GPR35A activity or levels. GPR35A polypeptides and
CC inappropriate GPR35A activity or levels. GPR35A polypeptides and
CC inappropriate GPR35A activity or levels. GPR35A polypeptides and
CC polymucleotides, agonists, antagonists and antibodies are used to treat:
CC polymucleotides, using it used:
CC polymucleotides activity or levels. GPR35A polypeptides and
CC polymucleotides in antagonists and antibodies are used to treat:
CC polymucleotides in uthary recention; cancer; diabetes; obeatty; anorexia;
CC hypertrophy; migraine; vomiting; psychotic and neurological disorders
CC dementia and severe mental retardation; and dyskinesias such as
CC Huntingdon's or Gilles de la Tourette's syndrome. The polynucleotide is
also useful as a source of primers and probes, and also for detecting the
                                  3352 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCCGTGCTAAGGCCCACAAAAGC 3411
                                                                                                                                                                                                                                                                                                                 GPR35A; hùman; G-protein coupled receptor; purinergic; 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic; cytostatic; antidabetic; ancectic; antiasthmatic; antiparkinsonian; hypotensive; osteopathic; antianginal; cardiant; cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic; tranquillizer; antidepressant; neuroleptic; nootropic; anticonvulsant; gene therapy; diagnosis; vaccine; ss.
                AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGCTCCCCGTGCTAAGGCCCACAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.
                                                                                                                                                                                                                                                                                    Human G-protein coupled receptor GPR35A cDNA
                                                                                              CAGGACTCTCTGTGCGTGACCCTCGCCTAA 3441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                        AAZ35390 standard; cDNA; 1043 BP
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P-PSDB; AAY35390.
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                                      Length 1043;
C; 315 G; 206 T; 0 U; 0 Other;
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0; Mismatches 9;
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Local Similarity 99.0%;
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Search completed: February 11, 2006, 09:42:57 Job time : 691 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	DRSHT.H	ALIGNMENTS
Database : EST:*	AY401607	
	LOCUS	IRIPT, partial
3: gD_est3:* 4: gD_htc:* 5: gD_htc:*	ACCESSION	947401607.1 GI:39757596
	KEYWORDS	GSS. Homo sapiens (human)
	ORGANISM	Homo saprems Buberonts: Motazos Chordara: Craniata: Vertebrata: Buteleostomi;
: gb gss1:* 0: gb gss2:*	<b>.</b>	hammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.
יירספא"תה ידד	REFERENCE	1 (bases 1 to 930)
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	AUTHORS	Clark A.G., Glanowski, S., Micison, K., Incluse, F., Kojailmai, C., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
SUMMARIES	TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous
one ro	JOURNAL	gene trios Science 302 (5652), 1960-1963 (2003)
Score Match Length DB ID Description	PUBMED REFERENCE	14671302 2 (bases 1 to 930)
922 99.1 930 10 AY401607 AY401607 Homo sapi	AUTHORS	<pre>Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,</pre>
72.5 906 7 CM335542 CM335542		<pre>Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams M.D. and Caroill.M.</pre>
65.6 960 7 CN843697 CN843597 64.6 750 7 CO921772 CO921772	TITLE	Direct Submission
63.6 642 10	JOURNAL	Submitted (16-NOV-2003) Lelera Genomics, *3 West Gude Dire; Rockville, MD 20850, USA
61.4 759 7 C0957219 C0957219	COMMENT	This sequence was made by sequencing genomic exons and ordering
924 10 AY401609 AY401609 2649 4 AK036503 AK036503	FEATURES	Location/Qualifiers
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7 CN832122	gene	<pre>&lt;1&gt;930 /gene="GPR35"</pre>
.4 54.9 1009 2 BB609892 BB609892		/locus_tag="HCM0947"
499.2 53.7 855 7 CN832152 CN832152 AGENCOURT	ORIGIN	
415 44.6 827 7 CN843490 CN843490	Query Match	Query Match 99.1%; Score 922; DB 10; Length 930;
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Hominidae; Homo.

12 (bases 1 to 876)

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                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Homo sapiens
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CN834209 876 bp mRNA linear EST 02-JUN-2004 AGENCOURT 15864200 NIH MGC_145 Homo sapiens cDNA clone IMAGE:7001934 3', mRNA sequence.
CN834209.1 GI:47938609

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GGGCAGGCAGGCCACCCGCAAGGCTAAACGCATGGTCTGGGCCCAACCTCCTGGTGTTC 678
                                                                               GTGGTCTGCTTCCTGCCCCTGCACGTGGGGCTGACAGTGCGCCTCGCAGTGGGCTGGAAC 738
                                                                                                            GCCTGTGCCCTCCTGGACGATCCGTCGCGCCCTGTACATAACCAGCAAGCTCTCAGAT 798
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                                                                                                                                           GCCAACTGCTGCTGGACGCCATCTGCTACTACATGGCCAAGGAGTTCCAGGAGGCG
                      /organism="Homo sapiens"
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db_xref="taxon:9606"
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/issue_type="mixed"
/lab host="DH10B"
/clone_lib="NIH_MGC_145"
                                                                                                                                                                                                                                                                                       CN835542.1 GI:47941197
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Homo sapiens
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/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1; by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ECGNV-XmnI/KhoI-3', 5'-ECGNV-XmnI/KhoI-3', For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnln.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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AGENCOURT 30698404 NIH MGC_145 Homo sapiens cDNA clone
IMAGE: 211833 3', mRNA sequence.
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/lab_hogt="DH10B"
/lab_hogt="DH10B"
/clone lib="NHH WGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; Order with WGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-Xmn1/Xhol-3', S'-EcoRV-Xmn1/Xhol-3', S'-EcoRV-Xmn1/Xhol-3', Por information about which gene each clones represents, please visit our anonymous ftp site at
                         213 GCTGACAGTGCGCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCG 154
                                                                                                                                                                                                                                                                                             768 GGCCCTGTACATAACCAGCAAGCTCTCAGATGCCAACTGCTGCCTGGACGCCATCTGCTA 827
                                                                                                                                                                                                                                                                                                                    153 CGCCCTGTACATAACCAGCAAGCTCTCAGATGCCAACTGCTGCCTGGACGCCATCTGCTA 94
                                                                                                                                                                                                                                                                                                                                                                                                          93 CTACTACATGGCCAAGGAGTTCCAGGAGGCGTCTGCACTGGCCGTGGCTCCCAGTGCTAA 34
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
Bldg. 31 Rml0AD/Betheada, MD 20892
Rmail: cgapbs-r@mail.inh.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at:
http://image.llnl.gov
Plate: IRBIS row: d column: 11
High quality sequence stop: 407.
Location/Qualifiers
1. 750
//db_xref="taxon:806"
//db_xref="taxon:806"
//db_xref="taxon:8066"
                                                                                                               273 ccacardercradeccaaccrecregrerregregrerecrecrececerecaeges
                                                                                                                                                                                                     708 GCTGACAGTGCGCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCCTGGAGACGATCCGTCG
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1 (bases 1 to 750)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           888 GGCCCACAAAAGCCAGGACTCTCTGTGCG 916
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C0921772.1 GI:51272514
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1. (Dases 1 to 960)

2. NIH-MGC http://mgc.nci.nih.gov/.

2. National Institutes of Health, Mammalian Gene Collection (MGC)

3. NIH-MGC http://mgc.nci.nih.gov/.

3. Orntact: Daniela 8. Gerhard, Ph.D.

3. Contact: Daniela 8. Gerhard, Ph.D.

3. Contact: Daniela 8. Gerhard, Ph.D.

4. Contact: Daniela 8. Gerhard, Ph.D.

5. Contact: Daniela 8. Gerhard, Ph.D.

6. Confect Genomics

8. Mational Cancer Testitute / NIH

8. Highs I Rml0A07 Bethesda, MD 20892

8. Email: cgapber-demail.nih.gov

7. Tissue Procurement: GPCR Consortium

6. Consortium

6. Consortium

6. Consortium

6. Consortium

7. Sequencing by: Agencourt Bioscience Corporation

6. Cond through the I.M.A.G.E. Consortium/LIML at:

8. High quality sequence stop: 568.

8. Location/Qualifiers

9. Location/Qualifiers

1. Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                  CN843697 960 bp mRNA linear EST
AGENCOURT 15864168 NIH_MGC 145 Homo sapiens cDNA clone
IMAGE:7001932 3', mRNA sequence.
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                                                                                                             CN843697.1 GI:47949352
                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                Homo sapiens
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                                      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Diect Submission Cargill, M. Sibmisted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTGTTTCAGGAGCCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCTGCTGGGATTC
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Pred. No. 1.1e-118;
0; Mismatches 43; Indels 0;
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    .642
    /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

Science 302 (5652), 1960-1963 (2003)
14671302
                                                                                                                                                                                                                                                                                                                                         /gene="GPR35"
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milarity 93.3%;
Conservative 0
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Pan troglodytes GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,
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           ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."
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1 (bases 1 to 642)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Retriars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
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Pan troglodytes
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                          GTACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCCTTGCGGCA
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                                                                                                                       o'
                                                                                    DB 7; Length 750;
                                                                                                                       Indels
                                                                                  Score 601.2; DB 7;
Pred. No. 7.5e-121;
0; Mismatches 19;
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Matches 612; Conservative (
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                                                 301 TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC 360
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Mational Institutes of Health, Mammalian Gene Collection (MGC)

Motional Institutes of Health, Ph.D.

Contact: Daniels S. Gerhard, Ph.D.

Mational Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: capbbs-remail.inih.gov

Tissue Procurement: Guthrie cDNA Resource Center

CDNA Library Preparation: Guthrie cDNA Resource

CDNA Library Preparation: Guthrie cDNA Resource

CDNA Library Preparation: Guthrie cDNA Resource

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be therp://image.lnl.gov

http://mage.lnl.gov

http://mage.lnl.gov

Plate: IRBI7 row: h column: 12

High quality sequence start: 30

High quality sequence start: 30

High quality sequence stop: 639.

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Location/Qualifiers
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
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AGENCOURT 30842510 NIH_MGC_146 Homo sapiens cDNA clone IMAGE37389770 3', mRNA sequence.
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/lab host="host="mixer"
/lab host="bhiob"
/clone lib="winth MGC 145"
/clone lib="winth MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORPS were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/Xhol-3', 5'-EcoRV-XmnI/Noc1-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at this is a NIH MGC Library."

a Note: this is a NIH MGC Library."
                  EST 16-AUG-2004
                                                                                                                                                                                                                                                                                                     Hominidae; Homorate; busicinolicogilies; Filmates; Catarinin; Maminidae; Homorate; Deses 1 to 778)

S NIH-MGC http://mgc.nci.nih.gov/.

In Ubases 1 to 778)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S Gerhard, Ph.D.

Coffice of Cancer Genomics

National Cancer Institute / NIH

BldG: 31 RanioAo7 Betheeda, MD 20892

Email: Cgapbs-remail.nigov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINI

CONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINIA at:

http://mage.llhi.gov

Plate: IRBIS row: b column: 12

High quality sequence start: 33

Location/Qualifiers
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                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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AGENCOURT 30488658 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:2211810 5', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:7211810"
                                                                                                                                    C0923163.1 GI:51275314
                                                                                                                                                                                               Homo sapiens (human)
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1. .924
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                              /gene="GPR35"
/locus_tag="HCM0947"
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Best Local Similarity 77.7%;
Matches 704; Conservative
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Mus musculus GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogaba, Y., Tagawa, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

L. Submitted (16-ULL-201) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-reseger.riken.jp, WL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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15 (MGD|MGI:1929509, GB|NM_022320, evidence: BLASTN, 99%,
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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|db_xref="G1:26331446"
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/strain="C57BL/6J"
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                                                                                                           CTGCTGCCTGGATGCCATCTGTTACTACTAGGCCAGAGAGTTCCAGGAAGCGTCCAA 860
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2649)
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK036503 2649 bp mRNA linear HTC 03-APR-2
Mus musculus adult male bone CDNA, RIKEN full-length enriched
Library, clone:9830121M19 product:G protein-coupled receptor 35,
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High-efficiency full-length cDNA cloning
With-Enzymol. 303, 19-44 (1999)
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AK036503.1 GI:26331445
HTC; CAP trapper
Mus musculus (house mouse)
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Group Phase I is II Team.

Group Phase I is II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

As Good of 60,770 full-length cDNAs

As Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,

Ryukuda,S., Puruno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatu,N., Hanagaki,T., Haramach,T., Haramach,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Katoh,H., Saski,D., Shibata,K., Sakai,C., Sakai,C., Sakazume,N.,

Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohaoto,N.,

Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,F., Sano,H.,

Sagabe,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Muramatuku,M. and Hayashizaki,Y.

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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,

WELittpl://Genome-gsc.riken.jp/, Tel:81-45-503-9222,
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rmhomtetrlymtnlavadicilcsippvulysikxysssbtpvcqisqgiylanrymsi
sivtalavdryvavrhplrareirsprqaaavcvalmvivvtsivvrmrigmqeggpc
pssqtrrnpsttapsilgfylplalvypcslqvytvlsrrpaadvgqaeatqkathmv
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(S (MGD|MGI:1929509, GB|NM_022320, evidence: BLASTN, 99%,
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(dev_gtgge="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yujiwake, S., Imoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKRN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
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Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4254)
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1 (bases 1 to 783)

S NIH-MGC http://mgc.nci.nih.gov/.

In the mational Institutes of Health, Mammalian Gene Collection (MGC)

In the mational Institutes of Health, Mammalian Gene Collection (MGC)

In the mational Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

BldG. 31 RM10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lnl.gov

Plate: IRBI3 row: a column: 03

High quality sequence stop: 482.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                      744 TGCCCTCCTGGAGGACGATCCGTCGCGCCCTGTACATAACCAGCAAGCTCTCAGATGCCAA
CTGCTTCCTGCCCCTGCACGTGGGGCTGACAGTGCGCCTCGCAGTGGGCTGGAACGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CN835586 782 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:7001933 5', mRNA sequence.
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/cell type="N006821"
/clone lib="RIKEN full-length enriched mouse cDNA library"
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://genome.gsc.riken.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         627
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/strain="NOD"
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DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov
Plate: IRBIS row: b column: 12
High quality sequence stop: 478.

Location/Qualifiers

1. 717

Ab _xref="mtxx" | Ab _xref="mtxx" |

Ab _xref="btx | Ab _xref="btx |

Ab _xref="btx |
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Pred. No. 2.3e-102;
0; Mismatches 19;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapba-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                   9 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG
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0; Mismatches 29; Indels
                                           0; Mismatches
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AUTHORS
TITLE
JOURNAL
COMMENT
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538 491 478 551 418 611 358 179 298 731 238 791 178 851 118

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1. .1019
| organism="Homo sapiens"
| organism="Homo sapiens"
| organism="Homo sapiens"
| db_xref="ntaxon:9606"
| clone="INMAB:7001931"
| tissue_type="mixed"
| /lab_host="DH108"
| /lab_host="DH108"
| /lote="Vector: pcDNA3.1; Site 1: varies by clone; Site_2: varies by clone; pcDNA3.1; Site 1: varies by clone; DNFs were PCR-amplified and cloned into varies by clone; pcDNA3.1; Site_1: varies by clone; DNFs were PCR-amplified and cloned into varies by clone; DNFs were PCR-amplified and cloned into varies by clone and include the following: 5'-EcoRV-XmnI/Khol-3', S'-EcoRV-XmnI/Nocl-3', RcoRV (TA cloned, non-directional).
| For information about which gene each clones represents, please visit our anonymous ftp site at tp://image.llhl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                     Extracted; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (Dases 1 to 1019)

1 (Dases 1 to 1019)

1 (Dases 1 to 1019)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Unpublished (1999)

5 Contact: Daniels S. Gerhard, Ph.D.

6 Cfice of Cancer Genomics

7 National Cancer Institute / NIH

8 National Cancer Genomics

8 National Cancer Genomics

8 National Cancer Genomics

8 National Cancer Institute / NIH

8 National Cancer Institute / NIH

8 National Cancer Genomics

8 Mail: cgapbs-rémail.nih.gov

7 Tissue Procurement: GPCR Consortium

CDNA Library Preparation GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium information can be

1 Clone distribution: MGC clone distribution information can be

1 Clone distribution: a column: 01

8 High quality sequence stop: 474.

1 High quality sequence stop: 474.

1 High quality sequence etop: 474.
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AGENCOURT 15864152 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:7001931 3', mRNA sequence.
                                                                                                                      CN832122.1 GI:47935875
                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                      147 TAACCAGCAAGCTCTCAGAIGCCAACIGCIGCCTGGACGCCAICTGCTACTACTACACGA
                267 GGGCCAACCTCCTGGTGTTCGTGGTCTGCTTCCTGCCCCTGCACGGGGGGTGACAGTGC
                                                          719 GCCTCGCAGTGGGCTGGAACGCCTGTGCCCTCTGGAGACGATCCGTCGCCCTGTACA
 659 GGGCCAACCTCCTGGTGTTCGTGGTCTGCTTCCTGCCCCTGCACGTGGGGCTTGAACAGTGC
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 21, Appli Sequence 29, Appli Sequence 225, Appl Sequence 3, Appli Sequence 1, Appli Sequence 117, Appl Sequence 117, Appli Sequence 16, Appli Sequence 26, Appli Sequence 193, Appli Sequence 193, Appli Sequence 194, Appli Sequence 1, Appli Sequence 69, Appli Sequence 574, Appli Sequence 574, Appli Sequence 574, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli
SUMMARIES	US-09-422-869-1 US-09-422-869-1 US-09-170-496B-225 US-09-170-496B-225 US-09-170-496B-3 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-496B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117 US-09-170-66B-117
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Sequence 6, Appli Sequence 6, Appli	Sequence 3, Appli	Sequence 39, Appl		Sequence 540, App	Sequence 18, Appl	Sequence 1391, Ap	Sequence 1417, Ap	Sequence 22, Appl	Sequence 171, App	• •	Seguence 74, Appl	Sequence 27, Appl	Sequence 1, Appli	Sequence 1, Appli					
US-08-599-654-6 US-08-485-573-6	US-08-944-868A-6	US-08-944-423A-6	US-08-925-743-6	US-08-944-496-6	US-08-925-767-6	US-09-875-076-3	US-09-170-496D-39	US-09-170-496D-185	US-09-826-509-540	US-08-405-271A-18	US-09-016-434-1391	US-09-023-655-1417	US-10-087-345A-22	US-09-976-594-171	US-09-016-434-1482	US-09-814-915A-74	US-09-875-076-27	US-08-442-134A-1	US-08-444-581B-1
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87.8	87.8	87.8	87.8	87.8	87.8	87.6	87.4	87.4	86	86	98	98	98	98	85.6	85.6	83.8	82.4	82.4
25	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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121 GCGCTCTGGGTGTTCTGCTGCCGCATGCAGGACGGAGACCCGCATCTACATGACC 180
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Sequence 21, Application US/09422869

Sequence 21, Application US/09422869

Patent No. 6235481

GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: ODLONSKY, XUKIO
APPLICANT: ODLONSKY, VIKIO
APPLICANT: CAN, NANCHSA
APPLICANT: SREENNA, SRAWUS
APPLICANT: SREENNA, SRAWUS
APPLICANT: SREENNA, SRAWUS
APPLICANT: APRICANT: HANIS, CRAIG I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: HANIS, CRAIG I.
APPLICANT: HONSHING SABOR
APPLICANT: 1901.
APPLICANT: 1901.
APPLICANT: APPLICATION NUMBER: 0S/09/422,869
CURRENT FILING DATE: 1999-10-21
BEALIER APPLICATION NUMBER: 60/134,175

EARLIER PLING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENT VET.
INNYMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.0%; Score 920.4; DB 3; Length 1875; Best Local Similarity 99.4%; Pred. No. 2e-186; Matches 924; Conservative 0; Mismatches 6; Indels 0;
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Query Match
Best Local Similarity 99.4%;
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         ; TYPE: DNA
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                                                                    CGGCTGCGTGCCGCGGGGCTGCGGTCCCCCAGGCAGGCTGCGGCGGCGTGCGGGGGCGCTCCTC
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         CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGCATCTACCTGACCAACAGG
                                                        TACATGAGCATCAGCCTGGTCACGCCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCCAC
                                                                                                      CCGCTGCGTGCCCGCGGGCTGCCCCCCAGGCAGGCTGCGGCCCGTGTGCGCGGGTCCTC
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                                                                                                                                                                                                   TTCTGCTTCAGGAGCACCCGGCACAATTTCAACTCCATGCGGTTCCCGCTGCTGCGATTC
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US-09-422-869-1
US-09-422-869-1
US-09-422-869-1
I Sequence 1, Application US/09422869
Patent No. 623481
I GENERAL INFORMATION:
APPLICANT: HORINAM, YUKIO
J APPLICANT: ODA, NACHISA
APPLICANT: ODA, NACHISA
APPLICANT: CANU, YIN-PING
APPLICANT: ZRERNAN, SEAMUS
APPLICANT: ZRERNAN, REMUGH
I APPLICANT: ZRERNAN, REMUGH
I APPLICANT: HANIS, CRAIG L.
J APPLICANT: BAPLICANTON WHERE: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-05-13
RALLIER PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFWWARE: PATENTIN Ver. 2.0
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Score 920.4; DB 3;
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Sequence 3, Application US/09170496D

Patent No. 6555339

GENERAL INFORMATION:
APPLICANT Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: No. 655539-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: No. 655539-Endogenous, Constitutively Activated Human G Protein-TITLE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOUTWARRE: Patentin version 3.1
SEQ ID NO 3
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Neceptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 225
LENGTH: 1098
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                                                                                                                                                                                                                              APPLICANT: Wateon, James D
APPLICANT: Wateon, James D
APPLICANT: Wateon, James G.
TITLE OF INVENTION: Polymucleotides, polypeptides expressed
TITLE OF INVENTION: by the polymucleotides and methods for their use.
FILE REPERENCE: 11000-1050U1
CURRENT APPLICATION WUMBER: US/99/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.1e-14;
0; Mismatches 364;
                                                                                                                     ; Sequence 29, Application US/09724864; Parent No. 6380362; GENERAL INFORMATION:
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ilarity 50.4%;
Conservative
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Matches 201; Conservative
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; ORGANISM: Mouse
US-09-724-864-29
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CRGANISM: Homo
US-09-170-496D-225
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US-09-170-496D-225
                                                    RESULT 3
US-09-724-864-29
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US-09-016-434-1429

i Sequence 1429, Application US/09016434

j Patent No. 6500938

i GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jaffrey J. Seilhamer

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE 1 NOTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                         12;
                                                                                                                                                                         Length 1089;
                                                                                                                                                                      Score 111.2; DB 3; Length 1 Pred. No. 1.4e-14; 0; Mismatches 293; Indels
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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER REALABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                      12.0%;
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CRGANISM: Homo sapiens
US-09-170-496D-3
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Best Local Similarity
LENGTH: 1089
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
PILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zealer, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: 94-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1429:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
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Best Local Similarity 50.39
Matches 309, Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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; CLONE: 9598152
US-09-016-434-1429
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                                                                                    Sequence 1, Application US/09850948
Patent No. 6919176
GENERAL INFORMATION:
APPLICANT: An, Songahu
APPLICANT: An, Songahu
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer FILE REPERENCE: 018781-000300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT PILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 2.2
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OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)
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Best Local Similarity 50.3%; Pred. No. 1.6e-14;
Matches 309; Conservative 0; Mismatches 293;
    669
                            905 rccccarcereric 918
    GCTTCCTGCCCCTG
                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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NAME/KEY: CDS
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LENGTH: 2693
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US-09-850-948-1
                                                                    RESULT 7
US-09-850-948-1
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Sequence 117, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G I:
TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G I:
TITLE OF INVENTION: No. 655339-Endogenous, CONSTITUTION OF INVENTION: No. 655339-Endogenous, CONSERVICE: AERN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID. NO 117.
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APPLICANT: Derk J. Bergsma, Catherine B. Ellis
TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor TITLE OF INVENTION: HUVCT36
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATG50022
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
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LENGTH: 1597
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STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
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Patent No. 6919176

GENERAL INFORMATION:
APPLICANT: Yang, Jianxin
APPLICANT: Tal, Songzhu
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer FILLE REFERENCE: 018701-008300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 5
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Pred. No. 2.4e-14;
0; Mismatches 365; Indels 33; Gaps
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LOCATION: (1)..(1098)
OTHER INFORMATION: human G-protein coupled receptor 68 (GPR68, OGR1)
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
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Pred. No. 2.6e-14;
0; Mismatches 365; Indels
                                FILE REFERENCE: Aren0047
CURRENT APPLICATION NUMBER: US/09/364,425B
CURRENT APPLICATION NUMBER: US/094,879
PRIOR APPLICATION NUMBER: 60/094,879
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-04
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
NUMBER: OF SEQ ID NOS: 60
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.8%;
50.2%;
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Best Local Similarity 50.29
Matches 402; Conservative
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CORGANISM: Homo sapiens
US-09-364-425B-26
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Patent No. 6555339

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRN-0040
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 193
LENGTH:: 128
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US-09-170-496D-193
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Sequence 165, Application US/09170496D

Patent No. 6555339

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: No. 6555339-Endogenous, CONSTITUTION OF SERVICATION NUMBER: US/09/170,496D

CURRENT APPLICATION NUMBER: US/09/170,496D

CURRENT PILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 165

SEQ ID NO 165

TENGRAL 1000
1130 CTTCTCCCTCCTGCTCACCAGCTTCAACTGCGTCGCCCGTGCTCTACTGCTTCGT 1189
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11.8*; Score 109.6; DB 3; Length 1
Best Local Similarity 52.5*; Pred. No. 3e-14;
Matches 272; Conservative 0; Mismatches 234; Indels
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L', Sequence 193, Application US/09170496D
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US-09-170-496D-165
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947 cricocrereracacceccaesescrectrecerérecericecericecedecides 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGCGATCAAGCTGGGCTTCTACGCCTACGGCGTCCTGCTGGTGCTAGGCCTGCT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    827 GCTCAACGGGCTGGCGTGTACGTCTTCTGCTGCCGCCAACACAAGACACCCTCAGT 886
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840 CGTGCACCTCCTGCAGCGGACGCAGCCTGGGGGCCGCTCCCTGCAAGCAGTCTTTCCGCCA 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                        900 TGCCCACCCCTCACGGGCCACATTGTCAACCTCACGCCTTCTCCAACAGCTGC 954
                                                                           774 GTACATAACCAGCAAGCTCTCAGATGCCAACTGCTGCCTGGACGCCATCTGCTAC
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Pred. No. 2.9e-10;
0; Mismatches 290; Indels
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09041545

Sequence 1, Application US/09041545

Patent No. 6071719

GENERAL INFORMATION:
APPLICANT: BATHE, GANESH M.
APPLICANT: HALSEY, WENDY S.
APPLICANT: APPLICANT: APPLICANT S.
APPLICANT: P.O. BOX 980

STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,545
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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Best Local Similarity 50.4%;
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NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,0
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TELEX: 846169
INFORMATION FOR ESO ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1815 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-MAR-1
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTMARE: Patentin version 3.1
SEQ ID NO 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 CTGGGTGTTCTGCTGCCGCATGCAGCAGGACGGAGCCCGCATCTACATGACCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 gerédréaacarcaécrrececságaagardaccarcecegaecreracer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.8%; Score 91; DB 3; Length 1128;
Best Local Similarity 47.7%; Pred. No. 2.7e-10;
Matches 370; Conservative 0; Mismatches 390; Indels
                                                                                                                                                      Sequence 201, Application US/09170496D Patent No. 655539 GRNERAL INFORMATION: APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                   JS-09-170-496D-201
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Search completed: February 11, 2006, 06:07:54 Job time : 215 secs

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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			SUMMAKIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
	930	100.0	930	5	US-10-083-168-84	Sequence 84, Appl	
~	925.2	99.5	930	Ŋ	US-10-083-168-15	Sequence 15, Appl	
'n	925.2	99.5	930	ഗ	US-10-225-567A-491	Sequence 491, App	
4	925.2	99.5	930	æ	US-10-696-639-6	Sequence 6, Appli	
ß	920.4	99.0	1875	m	US-09-768-877-21	Sequence 21, Appl	
v	920.4	99.0	1875	Ŋ	US-10-157-031-350	Sequence 350, App	
7	920.4	99.0	49136	٣	US-09-768-877-1	Sequence 1, Appli	
60	919	98.8	1644	σ	US-10-505-486-186	186	
o	916.8	98.6	24477	ω	US-10-741-600-17827	Sequence 17827, A	
10	900	96.8	1989	9	US-10-101-510-636	Sequence 636, App	
11	439.2	47.2	9	10	US-11-060-756-1687	Sequence 1687, Ap	
12	439.2	47.2	9	10	US-11-060-756-5959	Sequence 5959, Ap	
13	200.6	21.6	201	æ	US-10-741-600-61537	Sequence 61537, A	
14	200.6	21.6	201	8	US-10-741-600-61547	Sequence 61547, A	
15	200.6	21.6	201	œ	US-10-741-600-61549	Sequence 61549, A	
16	200.6	21.6	201	80	US-10-741-600-61551	Sequence 61551, A	
17	200.6	21.6	201	œ	US-10-741-600-61552	Sequence 61552, A	
18	200.6	21.6	201	ω	US-10-741-600-61567	Sequence 61567, A	
19	200.6	21.6	201	80	US-10-741-600-61568	Sequence 61568, A	
20	197.4	21.2	201	8	US-10-741-600-61525	Sequence 61525, A	
21	197.4	21.2	201	œ	US-10-741-600-61532	Sequence 61532, A	
22	197.4	21.2	201	œ	US-10-741-600-61535	Sequence 61535, A	
23	195.8	21.1	201	œ	US-10-741-600-61565	Sequence 61565, A	

9	Sequence 61524, A	Sequence 596, App	Sequence 596, App	Sequence 225, App	Seguence 3, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 1429, Ap	Sequence 113, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 272, App	Sequence 113, App	Sequence 456, App	Sequence 23834, A	Sequence 2, Appli	Sequence 5, Appli	Sequence 147, App	Seguence 5, Appli	Sequence 117, App	Sequence 5, Appli
US-10-741-600-61546	US-10-741-600-61524	US-09-866-050A-596	US-10-152-661-596	US-10-251-385-225	US-10-251-385-3	US-10-267-811-1	US-10-101-510-17	US-10-305-720-1429	US-10-283-975A-113	US-09-850-948-1	US-10-273-575-1	US-10-225-567A-272	US-10-712-124-113	US-10-101-510-456	US-10-450-763-23834	US-10-167-192-2	US-10-400-991-5	US-10-505-486-147	US-09-850-948-5	US-10-251-385-117	US-10-273-575-5
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## ALIGNMENTS

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Sequence 84, Application US/10083168

Sequence 84, Application US/10083168

Sequence 84, Application US/10083168

Sequence 84, Application US.032033069A1

GENERAL INFORMATION:

APPLICANT: Liaw, Chen W.

APPLICANT: Behan, Dominic P.

APPLICANT: Behan, Dominic P.

APPLICANT: Behan, Dominic P.

APPLICANT: Applicant Marciejewski-Lenior, Dominique

APPLICANT: Leonard, James N.

APPLICANT: Leonard, James N.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Receptors

SOFTWARE ABEREROR'S AREA

UNMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 930
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Matches 930; Conservative
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                       Score 925.2; DB 5;
Pred. No. 4.3e-224;
0; Mismatches 3;
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                        Query Match
Best Local Similarity 99.7%;
Matches 927; Conservative
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           CGAGACACCTCAGACACGCCGCTGTGCCAGCTCTCCCAGGGCATCTACCTGACCAACAGG
                                                              TACATGAGCATCAGCCTGGTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC
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US-10-083-168-15
i Sequence 15, Application US/10083168
i Publication No. US20030023069A1
i GENERAL INFORMATION:
i APPLICANT: Liaw, Chen W.
i APPLICANT: Chalmers, Derek T.
i APPLICANT: Chalmers, Derek T.
i APPLICANT: Chalmers, Deminic P.
i APPLICANT: Chalmers, Deninic P.
i APPLICANT: Leonard, James N.
i APPLICANT: Leonard, James N.
i APPLICANT: Lin, I-Lin
i TITLE OF INVENTION: Endogenous And No. US2003
i TITLE OF INVENTION: Receptors
i TITLE OF INVENTION: Receptors
i TITLE OF INVENTION WIMBER: US/10/083,168
i CURRENT APPLICATION NUMBER: US/10/083,168
i SOUTHARE: Patentin version 3.1
seq ID NO 15
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ORGANISM: Homo sapiens
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Sequence 6, Application US/10696639
; Sequence 6, Application US/10696639
; Publication No. US20050037439A1
; Publication No. US20050037439A1
; GENERAL INFORMATION: OCTOPORATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERNTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: DOLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 0.1049/J.
; CURRENT APPLICATION NUMBER: US/10/696,639
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR APPLICATION NUMBER: 60/422,176
; NUMBER OF SEQ ID NOS: 3114
; SEQ ID NO 6: 300FWARE: PatentIn version 3.1
; LENGTH: 930
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                         ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGGACGCCATCTGCTACTACTACTACATGGCC
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        CTCGCAGTGGGCTGGAACGCCTGTGCCCTCGAGACGATCCGTCGCGCCCTGTACATA
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Pred. No. 4.3e-224;
0; Mismatches 3;
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Best Local Similarity 99.7
Matches 927; Conservative
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CORGANISM: homo sapiens
US-10-696-639-6
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US-10-696-639-6
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sequence 491, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
TILLE OF INVENTION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
FRIOR PELICALON NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
FRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SEQ ID NO 491
LENGTH: 930
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                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-10-225-567A-491
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APPLICANT: Baranova, A. V.
APPLICANT: Saranova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. F.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences FILE REPERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
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APPLICANT: SREENAN, SEAMUS
APPLICANT: SREENAN, SEAMUS
APPLICANT: CTANL, VIN-PING
APPLICANT: CTANL, CRAIG L.
APPLICANT: HANIS, CRAIG L.
APPLICANT: HANIS, CRAIG L.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARC.1307
CURRENT APPLICATION NUMBER: US/09/768,877
CURRENT APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALCHLIN Ver. 2.0
SEQ ID NO 21
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Pred. No. 7.1e-223;
0; Mismatches 6;
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Patent No. US20020150896A1
GENERAL INFORMATION:
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HORIKAMA, YUKIO
ODA, NACHISA
COX, NANCY J.
SREENAN, SEAMUS
ZHOU, YUN-PING
OTANI, KENICHI
HANIS, CRAIG I.
BELL, GRAEME I.
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Matches 924, Conservative
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CRGANISM: Human
US-09-768-877-21
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US-09-768-877-21
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APPLICANT:
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99.4%; Pred. No. 7.4e-223;
vative 0; Mismatches 6;
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US-09-768-877-1
Sequence 1, Application US/09768877
Sequence 1, Application US/09768877
Sequence 1, Goods 1
GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: ODA, NANCY J.
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: THUS:
APPLICANT: APPLICANT: GOAL OF THE TITLE OF THUS:
APPLICANT: APPLICANT: MENCH I.
APPLICANT: APPLICANT: WENCH I.
APPLICANT: APPLICANT: COALG I.
APPLICANT: APPLICANT: WENCH I.
CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR APPLICATION NUMBER: 09/422,869
SEQ ID NOS: 30
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SEQ ID NOS: 30
SEQ ID NOS: 30
1476 CAGGACTCTCTGTGCGTGACCCTCGCCTAA 1505
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Best Local Similarity 99.4
Matches 924; Conservative
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; ORGANISM: Human
US-09-768-877-1
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                                                                                                                   Length 1875;
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                                                                                                                99.0%; Score 920.4; DB 5;
99.4%; Pred. No. 7.1e-223;
tive 0; Mismatches 6;
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                       3.1
        NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version
SEQ ID NO 350
LENGTH: 1875
                                                                                                                   Query Match
Best Local Similarity 99.4
Matches 924; Conservative
                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-157-031-350
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Sequence 17827, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SEQ ID NO 17827

LENGTH: 24477
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; ORGANISM: Homo sapiens
US-10-741-600-17827
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Best Local Similarity 99.5%; Pred. No. 1.6e-222;
Matches 922; Conservative 0; Mismatches 5; Indels
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Squence 186, Application US/10505486

Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006FCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT APPLICATION NUMBER: J02-02-45728

PRIOR FILING DATE: 2002-02-22

PRIOR PAPLICATION NUMBER: JP 2002-213949

PRIOR PLING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: JP 2002-298237

PRIOR FILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-07-23

PRIOR PILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 233

SEQ ID NO 186
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ORGANISM: Human
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Best Local Similarity 99.2%; Pred. No. 1e-217;
Matches 925; Conservative 0; Mismatches 5; Indels
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PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 636
LENGTH: 1989
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                                                                                                                             , LUCUATION: (1912)
; OTHER INFORMATION: a, t, c, £
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1928)
; OTHER INFORMATION: a, t, c, g,
US-10-101-510-636
                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FBATURE:
NAME/KEY: modified_base
LOCATION: (1912)
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                   CTGGGCTTCTACGCCTACTTGGGCGTCCTGCTGGTGCTAGGCCTGCTGACAGCCTG
                                                                        GCGCTCTGGGTGTTCTGCTGCCGCATGCAGTGGACGGAGACCCGCATCTACATGACC
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Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF PILE REPERENCE: 15117-0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
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US-10-101-510-636
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Sequence 5959, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
BAPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, Wolliam Martin
APPLICANT: Wolliam Martin
APPLICANT: Wolliam Martin
APPLICANT: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Perentin version 3.2
ELENGTH: 600
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Publication No. US20050026169A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLOR01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 61537
LENGTH: 201
LENGTH: 201
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US-10-741-600-61537
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031896-042000)
CURRENT PEPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 1687
LENGTH: 600
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47.2%; Score 439.2; DB 10;
Best Local Similarity 99.3%; Pred. No. 3.1e-101;
Matches 441; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                            899 GCCAGGACTCTGTGCGTGACCCTCGCCTAA 930
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ORGANISM: Homo sapiens
US-11-060-756-1687
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US-11-060-756-1687
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RESULT 12 US-11-060-756-5959

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Publication No. US20050026169A1
GENERAL INFORMATION
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INPARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
                                                                                                                                                                                                                                                                                                                                                                  Sequence 61547, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REPERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61547
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Score 200.6; DB 8; Length 201;
Pred. No. 6.4e-41;
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Best Local Similarity 99.5
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; ORGANISM: Homo sapiens
US-10-741-600-61547
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US-10-741-600-61549
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US-10-741-600-61547
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Pred. No. 6.4e-41;
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NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 61549
LENGTH: 201
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Best Local Similarity 99.5%;
Matches 200; Conservative
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US-10-741-600-61549
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Sequence 29, Appl
Sequence 32790, A
Sequence 32790, A
Sequence 3110, Ap
Sequence 28, Appl
Sequence 13208, A
Sequence 15, Appl
Sequence 2954, Ap
Sequence 2554, Ap
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Sequence 321, App
Sequence 320, App
Sequence 61969, A
Sequence 13299, A
Sequence 13299, A
Sequence 36071, A
Sequence 36071, A
                                                                    February 11, 2006, 06:13:10; Search time 282 Seconds (without alignments) 2965.328 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-750-623-61969
US-10-750-623-36071
US-10-750-623-36071
US-11-127-877-29
US-11-127-877-29
US-11-135-27-3905
US-11-36-27-3100
US-11-36-27-3100
US-11-36-57-3100
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22, Appl 3778, Ap

Sequence Sequence

US-11.127-877-15 US-11.136-527-2954 US-11.136-527-2457 US-11.136-527-6553 US-11.127-877-22 US-11.136-527-3778

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APPLICANT: Merchiens, Pascal G.
APPLICANT: Hoffman, Marcel
APPLICANT: Apptraels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Methods, Compositions and Compound
FILE REFRENCE: P27,800-B USA
FURENT APPLICATION NUMBER: US/11/127,877
CURRENT APPLICATION NUMBER: 60/570,352
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 30
LEMETHE SET APPLICATION NUMBER: METHOR PRIOR PATENT NOW SEQ ID NOS: SOFTWARE: PATENT NOW SEQ ID NOS: SOFTWARE NOW SEQ ID NOS: SOFT
Sequence 463, App Sequence 3114, Ap Sequence 3025, Ap Sequence 3005, Ap Sequence 2011, Ap Sequence 3473, Ap Sequence 3473, Ap Sequence 3421, Ap Sequence 7225, Ap Sequence 1, Appli Sequence 9, Appli Sequence 1066, Ap Sequence 92, Appli Sequence 92, Appli Sequence 93, Appli Sequence 93, Appli Sequence 1066, Ap Sequence 1066, Appli Sequence 1066, Appli Appli Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 466, App
Sequence 466, App
Sequence 3152, Ap
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Pred. No. 3.7e-13;
0; Mismatches 365; Indels 33;
| US-11-136-527-463
| US-11-136-527-3314
| US-11-136-527-3314
| US-11-136-527-3005
| US-11-136-527-2101
| US-11-136-527-2101
| US-11-136-527-3442
| US-11-136-527-3442
| US-11-136-527-3442
| US-11-136-527-3129
| US-11-136-527-3129
| US-11-136-527-3129
| US-11-136-527-3129
| US-11-136-527-3129
| US-11-136-527-2066
| US-11-136-527-2064
| US-11-136-527-2064
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| US-11-136-527-3145
| US-11-136-527-3145
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GENERAL INFORMATION:
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US-11-127-877-30
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLOOLSS9

CURRENT APPLICATION NUMBER: 18/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 320

LENGTH: 1498
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257 GGTGGGCAACGCCCTGGTCATCTTCGTGATCCTTCGCTACGCAGGAGAAGAAGACGCTAC 316
                                                                                                                                           317 CAMCATCTACCTGCTCAACCTGGCCGTAGCCGACGAGCTCTTCATGCTGAGCGTGCCCTT
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9.64; Score 89; DB 7; Length 1498; cal Similarity 55.54; Pred. No. 5.1e-09;
217; Conservative 0; Mismatches 165; Indels
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US-10-995-561-320
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Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DEPECTION AND USES THEREOF
TITLE OF INVENTION: DEPECTION AND USES THEREOF
TITLE OF UNCENTION UNMER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SECTION OF SEC
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APPLICANT: MRI GENOMICS, INC.

APPLICANT: RERN, Richard

APPLICANT: RERN, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMIL100-2.

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR PLILING DATE: 2003-12-31

PRIOR APPLICANT: SOO-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENCE: 2002-12-31

SEQ ID NO 61969

LENGTH: 2095
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0; Mismatches 410; Indels
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                                                                                                                                Sequence 61969, Application US/10750185
Publication No. US20050260603A1
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; ORGANISM: Bovine 19866880917942
US-10-750-185-61969
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; Sequence 61969, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INPORMATION:
    APPLICANT: MAI GENOMICS, INC.
    APPLICANT: MAI GENOMICS, INC.
    APPLICANT: MAISE, Sue K.
    APPLICANT: RERK Richard
    APPLICANT: ROSENFELD, David
    APPLICANT: ROSENFELD, David
    APPLICANT: RATE, Stephen
    APPLICANT: PANTIN, Dennis
    APPLICANT: PANTIN, Dennis
    TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
    TITLE OF INVENTION: METHODS.
    FURRENT FILING DATE: 2003-12-31
    PRIOR FILING DATE: 2003-12-31
    PRIOR FILING DATE: 2003-12-31
    NUMBER OF SEQ ID NOS: 64922
    SOFTWARE: PATENTIN Version 3.1
    SEMPRICE: AND SECOND SECON
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599 AGAGGCCACCCACCGACGTGGGGCAGGCAGGCCACCCGCAAGGCTAAACGCATGGTCT
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APPLICANT: PMI GENOMICS, INC.

APPLICANT: RERR, Richard APPLICANT: ROBENPELD, David APPLICANT: ROBENPELD, David APPLICANT: BATES, Stephen APPLICANT: BATES, Stephen APPLICANT: BATES, Stephen APPLICANT: BATES, Stephen APPLICANT: MINITON: COMPOSITIONS FOR INPERRING BOVINE TRAITS ITLE OF INVENTION: COMPOSITIONS OR INFERENCE INMILION-2 CURRENT FILING DATE: 2003-12-31

PRIOR PILING DATE: 2002-12-31

PRIOR PILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALCATION VETSION 3.1
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Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                               5558 GGCCAAGCTCATCAACCTGGGCGTGTGGCTG 6588
                                                                                                                                                                                                                                                  396 GGCTGCGGCCGTGTGCGCGGTCCTCTGGGTG 426
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Publication No. US20050260603A1
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Best Local Similarity 49.3%;
Matches 265; Conservative
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US-10-750-185-36071/C
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Publication No. US20050272054A1
GRNERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO1559
CURRENT PILICHIO DATES: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5318 CAMCATCTACCTGCTCAACCTGGCCGTAGCCGAGCTCTTCATGCTGAGCGTGCCCTT 6377
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                                                                                                                                                                                                                                              539 TCTACCTGCCCCTGGCCGTGGTCTTCTGCTCCTGAAGGTGGTGACTGCCCTGGCCC 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               659 GGGCCAACCTCCTGGTGTTCGTGGTCTCCTGCC---CCTGCACGTGGGGGCTGACAG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCACGGCCATCGCCGT 335
953 ATGCGCTGAGCACAGGGCCTCAGCTGGGGGCGCTGCCCGCGTGGCCGGGGGTCTCTGGG--- 909
                                                                                     487
                                                                                                                                                             225 CGT-----GCTGCACTCCCTGCAGAC---ACCTCAGACACGCCGCTGTGCCAGCTCTC 275
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                                                                            428 TGGTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGATTCAGGAGGGGGGCTTCTGCT
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Pred. No.
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Best Local Similarity 55.5%;
Matches 217; Conservative
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US-10-995-561-13298
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                                         GGTGGGCTTCGTGTTGTACACTTTCCTCATGGGCTTCCTGCTGGCCGTCGGGGCCAT 797
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593
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: APPLICANT: PANTIN, Dennis
TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TILLE PRILICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION WESION 3.1
SEQ ID NOS: 64922
SOFTWARE PATENTING DATE: 2002-12-31
SOFTWARE PATENTING DATE: 2002-12-31
SOFTWARE PATENTING DATE: 2002-12-31
SOFTWARE PATENTING DATE: 2002-12-31
SEQ ID NOS: 64922
SOFTWARE PATENTING DATE: LENGTH: 1685
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9.5%; Score 88.2; DB 7; Length 1685;
Best Local Similarity 49.3%; Pred. No. 7.4e-09;
Matches 265; Conservative 0; Mismatches 263; Indels 9.
                                                                                                                                                                                                                                      Sequence 36071, Application US/10750623
Publication No. US20050287531A1
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ORGANISM: Bovine 19866880675545
                                                                                                                                                                                                          US-10-750-623-36071/c
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US-10-750-623-36071
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APPLICANT: Merchiers, Pascal G.
APPLICANT: Merchiers, Pascal G.
APPLICANT: Morfman, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Methods, Compositions and Compound Assays
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REPRENCE: P27,800-8 USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT PILING DATE: 2005-05-12
FRIOR APPLICATION NUMBER: 60/603,948
FRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin Version 3.3
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Pred. No. 4.3e-08;
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Sequence 29, Application US/11127877 Publication No. US20050287565A1 GENERAL INFORMATION:
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449 AGAGAGCAAGCTGCTTCTTGCTGTCTTCTACTGCATCCTGTTTGTATTTGGTCTTCTGGG 390
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8.0%; Score 74.2; DB 7; Length 7
Best Local Similarity 51.1%; Pred. No. 3.8e-06;
Matches 203; Conservative 0; Mismatches 188; Indels
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Bovine 19866880843412
US-10-750-185-32790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bovine 19866880843412
                                       SOFTWARE: PatentIN version 3.1
SEQ ID NO 32790
LENGTH: 706
NUMBER OF SEQ ID NOS: 64922
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US-10-750-623-32790/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 cracrecadcarcererrecreacerecareaderecacedereceregeserecrees 893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 GITCTGCTGCCGCATGCAGCAGTGGACGGAGACCCCGCATCTACATGACCAACCTGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CGCCTACTTGGGCGTCCTGCTGGTGCTAGGCCTGCTGCTCAACAGCCTGGGCGCTCTGGGT
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                                                                                                                                                                                                                                                                                                        APPLICANT: "Younte, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM.01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 3805
LENGTH: 2011
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APPLICANT: KERR Richard
APPLICANT: KOSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US 210,750,185
CURRENT FILLING DATE: 2003-12-31
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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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Publication No. U820050260603A1
GRNERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: CENOMICS, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                , Sequence 3805, Application US/11136527
, Publication No. US20050287570A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TYPE: DNA
1 ORGANISM: Rattus norvegicus
US-11-136-527-3805
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Best Local Similarity 52.14
Matches 201, Conservative
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US-10-750-185-32790/c
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                                                                                         US-11-136-527-3805
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RESERVENCE.
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HATES, Stephen
APPLICANT: PANTIN, Demis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMILLON 0-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PALENCE: APPLICATION VERSION 3.1
SEQ ID NO 32790
LENGTH: 706
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8.0%; Score 74.2; DB 7; Length 706;
Best Local Similarity 51.1%; Pred. No. 3.8e-06;
Matches 203; Conservative 0; Mismatches 188; Indels
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Publication No. US2005272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, MICHELE et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PAILNG DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRRESCO for Windows Version 4.0
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Best Local Similarity 51.0%; Pred. No. 9.4e-06;
Matches 203; Conservative 1; Mismatches 182; Indels
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CRGANISM: Homo sapiens
US-10-995-561-28
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LENGTH: 1428
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; Publication No. US20050287570A1
; Publication No. US20050287570A1
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-26
; PRIOR PAPLICATION NUMBER: US 60/574,294
; PRIOR PILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NOS: 31001
                  449 AGAGAGCAAGCTGCTTCTTGCTGTTCTTGCTGCATCCTGTTTGTATTTGGTCTTCTGGG 390
                                                                          CAACAGCCTGGCGCTCTGGGTGTTCTGCTGCCATGCAGCAGTGGACGGAGACCCGCAT 170
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Pred. No. 7.1e-06;
0; Mismatches 335; Indels 15;
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Sequence 13206, Application US/10995561
Publication No. US200502720541
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THERROF
TITLE OF INVENTION: DETECTION AND USES THERROF
TITLE OF INVENTION: DATE: 2004-11-24
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PASTERO for Windows Version 4.0
SEQ ID NO 13208
LENGTH: 13428
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603 TCGGGCACTACGCTGGGGCCCTCGCCTCGCAGGCCTTCTCTCTGCCTGGCAGTTTGGTT 662
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                                                                                                      663 GGTCGTAGCCGGCTGCCTCRTGCCCAACCTGTTCTTTG 700
                                                                          426 GCTGGTCATCGGCTCCCTGGTGGCTCGCTGCTCCTGG 463
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US-10-995-561-13208
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US-10-995-561-13208
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